SEQUENCE LISTING

<110> Cohen, Dalia et al.

<120> Identification of Genes Involved in
Alzheimer's Disease Using Drosophila Melanogaster

<130> 4-31612 A

<150> 60/236,893
<151> 2000-09-29

<150> 60/298,309
<151> 2001-06-14

<160> 53

<170> FastSEQ for Windows Version 4.0

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<211> 123
<212> DNA
<213> Homo Sapien

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tag 123

<210> 2
<211> 129
<212> DNA
<213> Homo Sapien

<400> 2
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gcagaagatg tgggttcaaa caaaggtgca atcattggac tcatggtggg cggtgttgtc 120
atagcgtag 129

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<211> 300
<212> DNA
<213> Homo Sapien

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atagcgacag tgatcgtcat caccttggtg atgctgaaga agaaacagta cacatccatt 180
catcatggtg tggtggaggt tgacgccgct gtcaccccag aggagcgcca cctgtccaag 240
atgcagcaga acggctacga aaatccaacc tacaagttct ttgagcagat gcagaactag 300

<210> 4

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<212> DNA
<213> Homo Sapien

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atagcgacag tgatcatcat caccttggtg atgctgaaga agaaacagta cacatccatt 180
catcatggtg tggtggaggt tgacgccgct gtcaccccag aggagcgcca cctgtccaag 240
atgcagcaga acggctacga aaatccaacc tacaagttct ttgagcagat gcagaactag 300

<210> 5
<211> 72
<212> DNA
<213> Homo Sapien

<400> 5
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acagtgcagg ca 72

<210> 6
<211> 1537
<212> DNA
<213> Homo Sapien

<400> 6
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gaattccacc caaggagcgg gcgcctggga tcagagcgtc ctgtttagca ataacggctg 180
gagcacgtcc tacaagttac gggagagtcg gctgtgaagg agacgttcgc ttatcccctg 240
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ttaataaatt ttccattttt tttcaaacaa gtatgaa 1537

<210> 7
<211> 332

<212> PRT
<213> Homo Sapien

<400> 7

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Ile Thr Ala Gly Ala Arg Pro Thr Ser Tyr Gly Arg Val Gly Cys Glu
            20                  25                  30
Gly Asp Val Arg Leu Ser Pro Val Ser Pro Leu Leu Ala Pro Pro Asp
        35                  40                  45
Pro Arg Leu Ala Ser Arg Trp Glu Gly Arg Ser Arg Met Lys Gly Lys
    50                  55                  60
Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu Asp Glu Asp Ser
65                  70                  75                  80
Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly Ser Gly Lys Arg
                85                  90                  95
Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln Ile Leu Arg Asp
            100                 105                 110
Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser Glu Gln Glu Lys
        115                 120                 125
Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu Gln Val Cys Asn
    130                 135                 140
Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp Met Leu Arg Lys
145                 150                 155                 160
Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg Arg Gly Ala Lys
                165                 170                 175
Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly Ile Lys Asn Phe
            180                 185                 190
Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys Thr Ala Gly Pro
        195                 200                 205
Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro Ser Ser Pro Gly
    210                 215                 220
Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr Thr Val Thr Ala
225                 230                 235                 240
Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val Gly Val Gly Gln
                245                 250                 255
Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe Thr Asp Thr Ser
            260                 265                 270
Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro Ser Thr Asn Thr
        275                 280                 285
Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro Pro Asp Leu Asn
    290                 295                 300
Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val Ala Leu Lys Arg
305                 310                 315                 320
Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala
                325                 330
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<210> 8
<211> 1053
<212> DNA
<213> Homo Sapien

<400> 8

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agtgctgtgc gcaaccacac ttaccagatg ttgacactgc tggcagagga ccgtgcagtt     120
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ccctcggccc ccacaggccc tgggcccctg ctggagtttg ctctgcacga ggatctgctg 180
acccgtgtgt tgacatggca gctgcaatgg gatgagcttg gggatggggt cgaggaacgg 240
cgggctgagc aactgaaact atttgaaatg ctagtgagcg aagctcgcca gccactgttg 300
cggcatggtc cagttcgtga ggctctgctc accctgctgg atgcctgtgg ccgccctgtg 360
cccagtagcc cagcactgga tgaaggcttg gtgctacttc tcagccagct gtgtgtttgt 420
gtggcccagg agccttcatt gctcgagttc ttcctgcagc cacctcctga gcctggagcc 480
gctccccgtc ttcttctctt ttctcgcctt gtccctttg tgcatcgaga gggcaccctg 540
ggccagcagg cccgtgatgc cctacttctt ctcatggctt tgtcagctgg gagccccact 600
gtgggccgct acatcgcgga tcactcttac ttctgcccgg tgctggccac agggctcagt 660
gccctgtact catcactgcc tcgaaagatt gaggttccag gggatgattg gcactgtctg 720
cgacgggaag actggctggg agtgccagcc cttgcactct tcatgagttc cctggagttc 780
tgcaatgcag taattcaggt ggctcacccc ctggtgcaga agcagttggt tgattatatc 840
cataatgggt tcctggtgcc tgtcatgggt cctgccttgc acaagacctc tgtggaggag 900
atgatcgcca gtaccgccta cctggaactt ttcctacgga gtatctcaga gcctgctttg 960
ctccgtacct tcctgcgatt cctgttgttg caccggcatg acacccacac catcctcgac 1020
accctcgttg ctcgtattgg cagtaactcc cgg 1053

<210> 9
<211> 351
<212> PRT
<213> Homo Sapien

<400> 9
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            20   25   30
Leu Leu Ala Glu Asp Arg Ala Val Pro Ser Ala Pro Thr Gly Pro Gly
        35   40   45
Pro Leu Leu Glu Phe Ala Leu His Glu Asp Leu Leu Thr Arg Val Leu
    50   55   60
Thr Trp Gln Leu Gln Trp Asp Glu Leu Gly Asp Gly Val Glu Glu Arg
65   70   75   80
Arg Ala Glu Gln Leu Lys Leu Phe Glu Met Leu Val Ser Glu Ala Arg
                85   90   95
Gln Pro Leu Leu Arg His Gly Pro Val Arg Glu Ala Leu Leu Thr Leu
            100   105   110
Leu Asp Ala Cys Gly Arg Pro Val Pro Ser Ser Pro Ala Leu Asp Glu
        115   120   125
Gly Leu Val Leu Leu Leu Ser Gln Leu Cys Val Cys Val Ala Gln Glu
    130   135   140
Pro Ser Leu Leu Glu Phe Phe Leu Gln Pro Pro Pro Glu Pro Gly Ala
145   150   155   160
Ala Pro Arg Leu Leu Leu Phe Ser Arg Leu Val Pro Phe Val His Arg
                165   170   175
Glu Gly Thr Leu Gly Gln Gln Ala Arg Asp Ala Leu Leu Leu Leu Met
            180   185   190
Ala Leu Ser Ala Gly Ser Pro Thr Val Gly Arg Tyr Ile Ala Asp His
        195   200   205
Ser Tyr Phe Cys Pro Val Leu Ala Thr Gly Leu Ser Ala Leu Tyr Ser
    210   215   220
Ser Leu Pro Arg Lys Ile Glu Val Pro Gly Asp Asp Trp His Cys Leu
225   230   235   240
Arg Arg Glu Asp Trp Leu Gly Val Pro Ala Leu Ala Leu Phe Met Ser
                245   250   255

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Ser Leu Glu Phe Cys Asn Ala Val Ile Gln Val Ala His Pro Leu Val
            260                 265                 270
Gln Lys Gln Leu Val Asp Tyr Ile His Asn Gly Phe Leu Val Pro Val
        275                 280                 285
Met Gly Pro Ala Leu His Lys Thr Ser Val Glu Glu Met Ile Ala Ser
    290                 295                 300
Thr Ala Tyr Leu Glu Leu Phe Leu Arg Ser Ile Ser Glu Pro Ala Leu
305                 310                 315                 320
Leu Arg Thr Phe Leu Arg Phe Leu Leu Leu His Arg His Asp Thr His
                325                 330                 335
Thr Ile Leu Asp Thr Leu Val Ala Arg Ile Gly Ser Asn Ser Arg
            340                 345                 350
```

<210> 10
<211> 1425
<212> DNA
<213> Homo Sapien

<400> 10

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gggaaagaaa atgaggcccc aggacacctg ggttcacacc caggtcccca gcgatgtctc      60
caccaccgct gctgcaaccc ctgctgctgc tgctgcctct gctgaatgtg gagccttccg     120
gggccacact gatccgcatc cctcttcatc gagtccaacc tggacgcagg atcctgaacc     180
tactgagggg atggagagaa ccagcagagc tccccaagtt gggggcccca tcccctgggg     240
acaagcccat cttcgtacct ctctcgaact acagggatgt gcagtatttt ggggaaattg     300
ggctgggaac gcctccacaa aacttcactg ttgcctttga cactggctcc tccaatctct     360
gggtcccgtc caggagatgc cacttcttca gtgtgccctg ctggttacac caccgatttg     420
atcccaaagc ctctagctcc ttccaggcca atgggaccaa gtttgccatt caatatggaa     480
ctgggcgggt agatggaatc ctgagcgagg acaagctgac tattggtgga atcaagggtg     540
catcagtgat tttcggggag gctctctggg agcccagcct ggtcttcgct tttgcccatt     600
ttgatgggat attgggcctc ggttttccca ttctgtctgt ggaaggagtt cggcccccga     660
tggatgtact ggtggagcag gggctattgg ataagcctgt cttctccttt tacctcaaca     720
gggaccctga agagcctgat ggaggagagc tggtcctggg gggctcggac ccggcacact     780
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agcgtgtgaa ggtgggccca gggctgactc tctgtgccaa gggctgtgct gccatcctgg     900
atacgggcac gtccctcatc acaggaccca ctgaggagat ccgggccctg catgcagcca     960
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tcatccagac tactcgaaat ggcgtccgcc tctgcttgtc cggtttccag gccctggatg    1140
tccctccgcc tgcagggccc ttctggatcc tcggtgacgt cttcttgggg acgtatgtgg    1200
ccgtcttcga ccgcggggac atgaagagca gcgcccgggt gggcctggcg cgcgctcgca    1260
ctcgcggagc ggacctcgga tggggagaga ctgcgcaggc gcagttcccc gggtgacgcc    1320
caagtgaagc gcatgcgcag cgggtggtcg cggaggtcct gctacccagt aaaaatccac    1380
tatttccatt gagcgaaaaa aaaaaaaaaa aaaaaaaaaa atcaa                    1425
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<210> 11
<211> 433
<212> PRT
<213> Homo Sapien

<400> 11

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            20                  25                  30
Glu Pro Ser Gly Ala Thr Leu Ile Arg Ile Pro Leu His Arg Val Gln
```

```
        35                  40                  45
Pro Gly Arg Arg Ile Leu Asn Leu Leu Arg Gly Trp Arg Glu Pro Ala
    50                  55                  60
Glu Leu Pro Lys Leu Gly Ala Pro Ser Pro Gly Asp Lys Pro Ile Phe
65                  70                  75                  80
Val Pro Leu Ser Asn Tyr Arg Asp Val Gln Tyr Phe Gly Glu Ile Gly
                85                  90                  95
Leu Gly Thr Pro Pro Gln Asn Phe Thr Val Ala Phe Asp Thr Gly Ser
            100                 105                 110
Ser Asn Leu Trp Val Pro Ser Arg Arg Cys His Phe Phe Ser Val Pro
        115                 120                 125
Cys Trp Leu His His Arg Phe Asp Pro Lys Ala Ser Ser Ser Phe Gln
    130                 135                 140
Ala Asn Gly Thr Lys Phe Ala Ile Gln Tyr Gly Thr Gly Arg Val Asp
145                 150                 155                 160
Gly Ile Leu Ser Glu Asp Lys Leu Thr Ile Gly Gly Ile Lys Gly Ala
                165                 170                 175
Ser Val Ile Phe Gly Glu Ala Leu Trp Glu Pro Ser Leu Val Phe Ala
            180                 185                 190
Phe Ala His Phe Asp Gly Ile Leu Gly Leu Gly Phe Pro Ile Leu Ser
        195                 200                 205
Val Glu Gly Val Arg Pro Pro Met Asp Val Leu Val Glu Gln Gly Leu
    210                 215                 220
Leu Asp Lys Pro Val Phe Ser Phe Tyr Leu Asn Arg Asp Pro Glu Glu
225                 230                 235                 240
Pro Asp Gly Gly Glu Leu Val Leu Gly Gly Ser Asp Pro Ala His Tyr
                245                 250                 255
Ile Pro Pro Leu Thr Phe Val Pro Val Thr Val Pro Ala Tyr Trp Gln
            260                 265                 270
Ile His Met Glu Arg Val Lys Val Gly Pro Gly Leu Thr Leu Cys Ala
        275                 280                 285
Lys Gly Cys Ala Ala Ile Leu Asp Thr Gly Thr Ser Leu Ile Thr Gly
    290                 295                 300
Pro Thr Glu Glu Ile Arg Ala Leu His Ala Ala Ile Gly Gly Ile Pro
305                 310                 315                 320
Leu Leu Ala Gly Glu Tyr Ile Ile Leu Cys Ser Glu Ile Pro Lys Leu
                325                 330                 335
Pro Ala Val Ser Phe Leu Leu Gly Gly Val Trp Phe Asn Leu Thr Ala
            340                 345                 350
His Asp Tyr Val Ile Gln Thr Thr Arg Asn Gly Val Arg Leu Cys Leu
        355                 360                 365
Ser Gly Phe Gln Ala Leu Asp Val Pro Pro Pro Ala Gly Pro Phe Trp
    370                 375                 380
Ile Leu Gly Asp Val Phe Leu Gly Thr Tyr Val Ala Val Phe Asp Arg
385                 390                 395                 400
Gly Asp Met Lys Ser Ser Ala Arg Val Gly Leu Ala Arg Ala Arg Thr
                405                 410                 415
Arg Gly Ala Asp Leu Gly Trp Gly Glu Thr Ala Gln Ala Gln Phe Pro
            420                 425                 430
Gly
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<210> 12
<211> 1242
<212> DNA

<213> Homo Sapien

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aaggatctca agctgatgaa aaaactggag cggcagcggg cacaggagga acaggcaaag 180
cgcctggaag aggaggaggc agcggcagag aaggaggacc gcgggcggcc ctacacactg 240
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gacagccccc accacatgcg tcaggatgag gaatccgagt tccgagaggg catcgtggtg 600
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caggtcactt gggacggacg ccaccagact tgtctccaaa aa 1242

<210> 13
<211> 381
<212> PRT
<213> Homo Sapien

<400> 13
Arg Cys Val Arg Asn Met Ala Glu Arg Gly Arg Lys Arg Pro Cys Gly
1 5 10 15
Pro Gly Glu His Gly Gln Arg Ile Glu Trp Arg Lys Trp Lys Gln Gln
20 25 30
Lys Lys Glu Glu Lys Lys Lys Trp Lys Asp Leu Lys Leu Met Lys Lys
35 40 45
Leu Glu Arg Gln Arg Ala Gln Glu Glu Gln Ala Lys Arg Leu Glu Glu
50 55 60
Glu Glu Ala Ala Ala Glu Lys Glu Asp Arg Gly Arg Pro Tyr Thr Leu
65 70 75 80
Ser Val Ala Leu Pro Gly Ser Ile Leu Asp Asn Ala Gln Ser Pro Glu
85 90 95
Leu Arg Thr Tyr Leu Ala Gly Gln Ile Ala Arg Ala Cys Ala Ile Phe
100 105 110
Cys Val Asp Glu Ile Val Val Phe Asp Glu Glu Gly Gln Asp Ala Lys
115 120 125
Thr Val Glu Gly Glu Phe Thr Gly Val Gly Lys Lys Gly Gln Ala Cys
130 135 140
Val Gln Leu Ala Arg Ile Leu Gln Tyr Leu Glu Cys Pro Gln Tyr Leu
145 150 155 160
Arg Lys Ala Phe Phe Pro Lys His Gln Asp Leu Gln Phe Ala Gly Leu
165 170 175
Leu Asn Pro Leu Asp Ser Pro His His Met Arg Gln Asp Glu Glu Ser
180 185 190

```
Glu Phe Arg Glu Gly Ile Val Val Asp Arg Pro Thr Arg Pro Gly His
        195                 200                 205
Gly Ser Phe Val Asn Cys Gly Met Lys Lys Glu Val Lys Ile Asp Lys
    210                 215                 220
Asn Leu Glu Pro Gly Leu Arg Val Thr Val Arg Leu Asn Gln Gln Gln
225                 230                 235                 240
His Pro Asp Cys Lys Thr Tyr His Gly Lys Val Val Ser Ser Gln Asp
                245                 250                 255
Pro Arg Thr Lys Ala Gly Leu Tyr Trp Gly Tyr Thr Val Arg Leu Ala
            260                 265                 270
Ser Cys Leu Ser Ala Val Phe Ala Glu Ala Pro Phe Gln Asp Gly Tyr
        275                 280                 285
Asp Leu Thr Ile Gly Thr Ser Glu Arg Gly Ser Asp Val Ala Ser Ala
    290                 295                 300
Gln Leu Pro Asn Phe Arg His Ala Leu Val Val Phe Gly Gly Leu Gln
305                 310                 315                 320
Gly Leu Glu Ala Gly Ala Asp Ala Asp Pro Asn Leu Glu Val Ala Glu
                325                 330                 335
Pro Ser Val Leu Phe Asp Leu Tyr Val Asn Thr Cys Pro Gly Gln Gly
            340                 345                 350
Ser Arg Thr Ile Arg Thr Glu Glu Ala Ile Leu Ile Ser Leu Ala Ala
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Leu Gln Pro Gly Leu Thr Gln Ala Gly Ala Arg His Thr
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<210> 14
<211> 1779
<212> DNA
<213> Homo Sapien

<400> 14

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gctcccgggg cgagcgcgca gccccgagcc cgccccgcgc ctcccggagc cctcccccc      180
gctgctccca tgcgcgcggg ctcgtccccg gccggcagca ccaagccttt tgtgcacgcc     240
gtgcccccct ctgacccct gcgccaggcc aaccgcctgc caatcaaggt gctgaagatg      300
ctgacggcac gaactggcca cattttgcac cccgagtacc tgcagccccc gccttccacg     360
ccggtcagcc ccatcgagct cgatgccaag aagagcccgc tggcgctgtt ggcgcaaaca     420
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cctttggccg gagcgtctcc gccgtccgtg atgacagcca gtttgtgccg ggacccttac    1140
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gcacatgatc cggctgctgc ggctgcggcg ctgaagtccg gatacccgct ggtgtacccc    1260
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cacgcctggc gcccccgtgc cggtgcccgc cgccaccgga ccgtactact ccccctacgc 1740
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<210> 15
<211> 593
<212> PRT
<213> Homo Sapien

<400> 15
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35 40 45
Arg Ala Arg Pro Ala Pro Pro Gly Ala Leu Pro Pro Ala Ala Pro Met
50 55 60
Arg Ala Gly Ser Ser Pro Ala Gly Ser Thr Lys Pro Phe Val His Ala
65 70 75 80
Val Pro Pro Ser Asp Pro Leu Arg Gln Ala Asn Arg Leu Pro Ile Lys
85 90 95
Val Leu Lys Met Leu Thr Ala Arg Thr Gly His Ile Leu His Pro Glu
100 105 110
Tyr Leu Gln Pro Leu Pro Ser Thr Pro Val Ser Pro Ile Glu Leu Asp
115 120 125
Ala Lys Lys Ser Pro Leu Ala Leu Leu Ala Gln Thr Cys Ser Gln Ile
130 135 140
Gly Lys Pro Asp Pro Ser Pro Ser Ser Lys Leu Ser Ser Lys Ser Gly
145 150 155 160
Phe Arg Val Pro Ser Ala Thr Cys Gln Pro Phe Thr Pro Arg Thr Gly
165 170 175
Ser Pro Ser Ser Ser Ala Ser Ala Cys Ser Pro Gly Gly Met Leu Ser
180 185 190
Ser Ala Gly Gly Ala Pro Glu Gly Lys Asp Asp Lys Lys Asp Thr Asp
195 200 205
Val Gly Gly Gly Gly Lys Gly Thr Gly Gly Ala Ser Ala Glu Gly Gly
210 215 220
Pro Thr Gly Leu Ala His Gly Arg Ile Ser Cys Gly Gly Gly Ile Asn
225 230 235 240
Val Asp Val Asn Gln His Pro Asp Gly Gly Pro Gly Gly Lys Ala Leu
245 250 255
Gly Ser Asp Cys Gly Gly Ser Ser Gly Ser Ser Ser Gly Ser Gly Pro
260 265 270
Ser Ala Pro Thr Ser Ser Ser Val Leu Gly Ser Gly Leu Val Ala Pro
275 280 285
Val Ser Pro Tyr Lys Pro Gly Gln Thr Val Phe Pro Leu Pro Pro Ala
290 295 300
Gly Met Thr Tyr Pro Gly Ser Leu Ala Gly Ala Tyr Ala Gly Tyr Pro
305 310 315 320
Pro Gln Phe Leu Pro His Gly Val Ala Leu Asp Pro Thr Lys Pro Gly
325 330 335

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Ser Leu Val Gly Ala Gln Leu Ala Ala Ala Ala Ala Gly Ser Leu Gly
            340                 345                 350
Cys Ser Lys Pro Ala Gly Ser Ser Pro Leu Ala Gly Ala Ser Pro Pro
        355                 360                 365
Ser Val Met Thr Ala Ser Leu Cys Arg Asp Pro Tyr Cys Leu Ser Tyr
    370                 375                 380
His Cys Ala Ser His Leu Ala Gly Ala Ala Ala Ala Ser Ala Ser Cys
385                 390                 395                 400
Ala His Asp Pro Ala Ala Ala Ala Ala Ala Leu Lys Ser Gly Tyr Pro
                405                 410                 415
Leu Val Tyr Pro Thr His Pro Leu His Gly Val His Ser Ser Leu Thr
            420                 425                 430
Ala Ala Ala Ala Ala Gly Ala Thr Pro Pro Ser Leu Ala Gly His Pro
        435                 440                 445
Leu Tyr Pro Tyr Gly Phe Met Leu Pro Asn Asp Pro Leu Pro His Ile
    450                 455                 460
Cys Asn Trp Val Ser Ala Asn Gly Pro Cys Asp Lys Arg Phe Ala Thr
465                 470                 475                 480
Ser Glu Glu Leu Leu Ser His Leu Arg Thr His Thr Ala Phe Pro Gly
                485                 490                 495
Thr Asp Lys Leu Leu Ser Gly Tyr Pro Ser Ser Ser Ser Met Ala Ser
            500                 505                 510
Ala Ala Ala Ala Ala Met Ala Cys His Met His Ile Pro Thr Ser Gly
        515                 520                 525
Ala Pro Gly Ser Pro Gly Asp Ala Gly Ala Ala Gln Pro Pro Pro Arg
    530                 535                 540
Ala Gly Thr Gln Gln Pro Leu Pro Pro Leu Leu Gln Glu Pro Ala Ser
545                 550                 555                 560
His Ala Trp Arg Pro Arg Ala Gly Ala Arg Arg His Arg Thr Val Leu
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Leu Pro Leu Arg Pro Leu Arg Thr Glu Thr Asp His Arg Leu Gly Ala
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Gly
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<210> 16
<211> 1938
<212> DNA
<213> Homo Sapien

<400> 16

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cggcactccc gcagtccagc cggctcctct agcccggcca cggctccgct gcgggccacc     180
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gcgccagctc ctcctcctcc cgctgctcct gctcccgggg cgagcgcgca gccccgagcc     300
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gccggcagca ccaagccttt tgtgcacgcc gtgccccccc ctgacccccc gcgccaggcc     420
aaccgcctgc caatcaaggt gctgaagatg ctgacggcac gaactggcca cattttgcac     480
cccgagtacc tgcagccccc gccttccacg ccggtcagcc ccatcgagct cgatgccaag     540
aagagcccgc tggcgctgtt ggcgcaaaca tgttcgcaga tcgggaagcc cgacccctcg     600
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ctgtcctcgg ccgggggtgc cccggagggc aaggacgaca agaaagacac cgacgtgggc     780
ggcggtggca agggcaccgg gggcgcctcg gccgaagggg gacccacggg gctggcacac     840
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taccacccct actccaagag cccgcttccc acgcctggcg cccccgtgcc ggtgcccgcc 1860
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<210> 17
<211> 645
<212> PRT
<213> Homo Sapien

<400> 17
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Pro Arg Arg Thr Pro Arg Ala Ala Arg His Ser Arg Ser Pro Ala Gly
35 40 45
Ser Ser Ser Pro Ala Thr Ala Pro Leu Arg Ala Thr Gln Asp Tyr Ser
50 55 60
Arg Leu Ala Pro Gly Ala Glu Lys Ala Arg Trp Ala Pro Val Ala Ala
65 70 75 80
Ala Pro Ala Pro Pro Pro Pro Ala Ala Pro Ala Pro Gly Ala Ser Ala
85 90 95
Gln Pro Arg Ala Arg Pro Ala Pro Pro Gly Ala Leu Pro Pro Ala Ala
100 105 110
Pro Met Arg Ala Gly Ser Ser Pro Ala Gly Ser Thr Lys Pro Phe Val
115 120 125
His Ala Val Pro Pro Ser Asp Pro Leu Arg Gln Ala Asn Arg Leu Pro
130 135 140
Ile Lys Val Leu Lys Met Leu Thr Ala Arg Thr Gly His Ile Leu His
145 150 155 160
Pro Glu Tyr Leu Gln Pro Leu Pro Ser Thr Pro Val Ser Pro Ile Glu
165 170 175
Leu Asp Ala Lys Lys Ser Pro Leu Ala Leu Leu Ala Gln Thr Cys Ser
180 185 190
Gln Ile Gly Lys Pro Asp Pro Ser Pro Ser Ser Lys Leu Ser Ser Lys
195 200 205
Ser Gly Phe Arg Val Pro Ser Ala Thr Cys Gln Pro Phe Thr Pro Arg
210 215 220
Thr Gly Ser Pro Ser Ser Ser Ala Ser Ala Cys Ser Pro Gly Gly Met

225 230 235 240
Leu Ser Ser Ala Gly Gly Ala Pro Glu Gly Lys Asp Asp Lys Lys Asp
245 250 255
Thr Asp Val Gly Gly Gly Gly Lys Gly Thr Gly Gly Ala Ser Ala Glu
260 265 270
Gly Gly Pro Thr Gly Leu Ala His Gly Arg Ile Ser Cys Gly Gly Gly
275 280 285
Ile Asn Val Asp Val Asn Gln His Pro Asp Gly Gly Pro Gly Gly Lys
290 295 300
Ala Leu Gly Ser Asp Cys Gly Gly Ser Ser Gly Ser Ser Ser Gly Ser
305 310 315 320
Gly Pro Ser Ala Pro Thr Ser Ser Ser Val Leu Gly Ser Gly Leu Val
325 330 335
Ala Pro Val Ser Pro Tyr Lys Pro Gly Gln Thr Val Phe Pro Leu Pro
340 345 350
Pro Ala Gly Met Thr Tyr Pro Gly Ser Leu Ala Gly Ala Tyr Ala Gly
355 360 365
Tyr Pro Pro Gln Phe Leu Pro His Gly Val Ala Leu Asp Pro Thr Lys
370 375 380
Pro Gly Ser Leu Val Gly Ala Gln Leu Ala Ala Ala Ala Ala Gly Ser
385 390 395 400
Leu Gly Cys Ser Lys Pro Ala Gly Ser Ser Pro Leu Ala Gly Ala Ser
405 410 415
Pro Pro Ser Val Met Thr Ala Ser Leu Cys Arg Asp Pro Tyr Cys Leu
420 425 430
Ser Tyr His Cys Ala Ser His Leu Ala Gly Ala Ala Ala Ala Ser Ala
435 440 445
Ser Cys Ala His Asp Pro Ala Ala Ala Ala Ala Ala Leu Lys Ser Gly
450 455 460
Tyr Pro Leu Val Tyr Pro Thr His Pro Leu His Gly Val His Ser Ser
465 470 475 480
Leu Thr Ala Ala Ala Ala Ala Gly Ala Thr Pro Pro Ser Leu Ala Gly
485 490 495
His Pro Leu Tyr Pro Tyr Gly Phe Met Leu Pro Asn Asp Pro Leu Pro
500 505 510
His Ile Cys Asn Trp Val Ser Ala Asn Gly Pro Cys Asp Lys Arg Phe
515 520 525
Ala Thr Ser Glu Glu Leu Leu Ser His Leu Arg Thr His Thr Ala Phe
530 535 540
Pro Gly Thr Asp Lys Leu Leu Ser Gly Tyr Pro Ser Ser Ser Ser Met
545 550 555 560
Ala Ser Ala Ala Ala Ala Ala Met Ala Cys His Met His Ile Pro Thr
565 570 575
Ser Gly Ala Pro Gly Ser Pro Gly Thr Leu Ala Leu Arg Ser Pro His
580 585 590
His Ala Leu Gly Leu Ser Ser Arg Tyr His Pro Tyr Ser Lys Ser Pro
595 600 605
Leu Pro Thr Pro Gly Ala Pro Val Pro Val Pro Ala Ala Thr Gly Pro
610 615 620
Tyr Tyr Ser Pro Tyr Ala Leu Tyr Gly Gln Arg Leu Thr Thr Ala Ser
625 630 635 640
Ala Leu Gly Tyr Gln
645

<210> 18

<211> 4022
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(4022)
<223> n = A,T,C or G

<400> 18
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gctgcagccc ggcaactttt ctgctgacga ggccggggcg cagctcttcg cgcagagcta 180
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aaggcgggga gagccatcct ccagttttac ccgaaatacg tggaactcat caaccaggct 2460
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ctgctgcccg tgcctcctga gttctggaac aagtcgatgc tggagaagcc aaccgacggg    2880
cgggaggtgg tctgccacgc ctcggcctgg gacttctaca acggcaagga cttccggatc    2940
aagcagtgca ccaccgtgaa cttggaggac ctggtggtgg cccaccacga aatgggccac    3000
atccagtatt tcatgcagta caaagactta cctgtggcct tgagggaggg tgccaacccc    3060
ggcttccatg aggccattgg ggacgtgcta gccctctcag tgtctacgcc caagcacctg    3120
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atgaagatgg cccttgacaa gatcgccttt atccccttca gctacctcgt cgatcagtgg    3240
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cacgggcccc agttcggctc cgaggtggag ctgagacact cctgaggtga cccggctggg    3960
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gg                                                                   4022
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<210> 19
<211> 1265
<212> PRT
<213> Homo Sapien

<220>
<221> VARIANT
<222> (1)...(1265)
<223> Xaa = Any Amino Acid

<400> 19

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His His Arg Gly Glu Xaa Xaa Arg Arg Gln Glu Glu Ala Ala Leu Leu
        35                  40                  45
Ser Gln Glu Phe Ala Glu Ala Trp Gly Gln Lys Ala Lys Glu Leu Tyr
    50                  55                  60
Glu Pro Ile Trp Gln Asn Phe Thr Asp Pro Gln Leu Arg Arg Ile Ile
65                  70                  75                  80
Gly Ala Val Arg Thr Leu Gly Ser Ala Asn Leu Pro Leu Ala Lys Arg
                85                  90                  95
Gln Gln Tyr Asn Ala Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr
            100                 105                 110
Ala Lys Val Cys Leu Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp
        115                 120                 125
Pro Asp Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu
    130                 135                 140
Leu Phe Ala Trp Glu Gly Trp His Asn Ala Ala Gly Ile Pro Leu Lys
145                 150                 155                 160
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Pro Leu Tyr Glu Asp Phe Thr Ala Leu Ser Asn Glu Ala Tyr Lys Gln
165 170 175
Asp Gly Phe Thr Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Asn Ser
180 185 190
Pro Thr Phe Glu Asp Asp Leu Glu His Leu Tyr Gln Gln Leu Glu Pro
195 200 205
Leu Tyr Leu Asn Leu His Ala Phe Val Arg Arg Ala Leu His Arg Arg
210 215 220
Tyr Gly Asp Arg Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu
225 230 235 240
Leu Gly Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val
245 250 255
Val Pro Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Leu
260 265 270
Gln Gln Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe
275 280 285
Phe Thr Ser Leu Glu Leu Ser Pro Met Pro Pro Glu Phe Trp Glu Gly
290 295 300
Ser Met Leu Glu Lys Pro Ala Asp Gly Arg Glu Val Val Cys His Ala
305 310 315 320
Ser Ala Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys
325 330 335
Thr Arg Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly
340 345 350
His Ile Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu Pro Val Ser Leu Arg
355 360 365
Arg Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala
370 375 380
Leu Ser Val Ser Thr Pro Glu His Leu His Lys Ile Gly Leu Leu Asp
385 390 395 400
Arg Val Thr Asn Asp Thr Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met
405 410 415
Ala Leu Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln
420 425 430
Trp Arg Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn
435 440 445
Phe Asp Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro
450 455 460
Val Thr Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Val
465 470 475 480
Pro Asn Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln
485 490 495
Phe Gln Phe His Glu Ala Leu Cys Lys Glu Ala Gly Tyr Glu Gly Pro
500 505 510
Leu His Gln Cys Asp Ile Tyr Arg Ser Thr Lys Ala Gly Ala Lys Leu
515 520 525
Arg Lys Val Leu Gln Ala Gly Ser Ser Arg Pro Trp Gln Glu Val Leu
530 535 540
Lys Asp Met Val Gly Leu Asp Ala Leu Asp Ala Gln Pro Leu Leu Lys
545 550 555 560
Tyr Phe Gln Pro Val Thr Gln Trp Leu Gln Glu Gln Asn Gln Gln Asn
565 570 575
Gly Glu Val Leu Gly Trp Pro Glu Tyr Gln Trp His Pro Pro Leu Pro
580 585 590
Asp Asn Tyr Pro Glu Gly Ile Asp Leu Val Thr Asp Glu Ala Glu Ala

595 600 605
Ser Lys Phe Val Glu Glu Tyr Asp Arg Thr Ser Gln Val Val Trp Asn
610 615 620
Glu Tyr Ala Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu
625 630 635 640
Thr Ser Lys Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr
645 650 655
Leu Lys Tyr Gly Thr Gln Ala Arg Lys Phe Asp Val Asn Gln Leu Gln
660 665 670
Asn Thr Thr Ile Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Glu Arg
675 680 685
Ala Ala Leu Pro Ala Gln Glu Leu Glu Glu Tyr Asn Lys Ile Leu Leu
690 695 700
Asp Met Glu Thr Thr Tyr Ser Val Ala Thr Val Cys His Pro Asn Gly
705 710 715 720
Ser Cys Leu Gln Leu Glu Pro Asp Leu Thr Asn Val Met Ala Thr Ser
725 730 735
Arg Lys Tyr Glu Asp Leu Leu Trp Ala Trp Glu Gly Trp Arg Asp Lys
740 745 750
Ala Gly Arg Ala Ile Leu Gln Phe Tyr Pro Lys Tyr Val Glu Leu Ile
755 760 765
Asn Gln Ala Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp
770 775 780
Arg Ser Met Tyr Glu Thr Pro Ser Leu Glu Gln Asp Leu Glu Arg Leu
785 790 795 800
Phe Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg
805 810 815
Arg Ala Leu His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly
820 825 830
Pro Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser
835 840 845
Asn Ile Tyr Asp Leu Val Val Pro Phe Pro Ser Ala Pro Ser Met Asp
850 855 860
Thr Thr Glu Ala Met Leu Lys Gln Gly Trp Thr Pro Arg Arg Met Phe
865 870 875 880
Lys Glu Ala Asp Asp Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro
885 890 895
Pro Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg
900 905 910
Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp
915 920 925
Phe Arg Ile Lys Gln Cys Thr Thr Val Asn Leu Glu Asp Leu Val Val
930 935 940
Ala His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp
945 950 955 960
Leu Pro Val Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala
965 970 975
Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His
980 985 990
Ser Leu Asn Leu Leu Ser Ser Glu Gly Gly Ser Asp Glu His Asp Ile
995 1000 1005
Asn Phe Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe
1010 1015 1020
Ser Tyr Leu Val Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile
1025 1030 1035 1040

Thr Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr
1045 1050 1055
Gln Gly Leu Cys Pro Pro Val Pro Arg Thr Gln Gly Asp Phe Asp Pro
1060 1065 1070
Gly Ala Lys Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe
1075 1080 1085
Val Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Gln Ala
1090 1095 1100
Ala Gly His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys
1105 1110 1115 1120
Glu Ala Gly Gln Arg Leu Ala Thr Ala Met Lys Leu Gly Phe Ser Arg
1125 1130 1135
Pro Trp Pro Glu Ala Met Gln Leu Ile Thr Gly Gln Pro Asn Met Ser
1140 1145 1150
Ala Ser Ala Met Leu Ser Tyr Phe Lys Pro Leu Leu Asp Trp Leu Arg
1155 1160 1165
Thr Glu Asn Glu Leu His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Asn
1170 1175 1180
Trp Thr Pro Asn Ser Ala Arg Ser Glu Gly Pro Leu Pro Asp Ser Gly
1185 1190 1195 1200
Arg Val Ser Phe Leu Gly Leu Asp Leu Asp Ala Gln Gln Ala Arg Val
1205 1210 1215
Gly Gln Trp Leu Leu Leu Phe Leu Gly Ile Ala Leu Leu Val Ala Thr
1220 1225 1230
Leu Gly Leu Ser Gln Arg Leu Phe Ser Ile Arg His Arg Ser Leu His
1235 1240 1245
Arg His Ser His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His
1250 1255 1260
Ser
1265

<210> 20
<211> 954
<212> DNA
<213> Homo Sapien

<400> 20
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ggacgcggtg cgcaaatccc tgcaaggggt ggcaggtgtc caggatgtgg aggtgcactt 180
ggaggaccag atggtcttgg tacacaccac tctacccagc caggaggtgc aggctctcct 240
ggaaggcacg gggcggcagg cggtactcaa gggcatgggc agcggccagt tgcagaatct 300
gggggcagca gtggccatcc tgggggggcc tggcaccgtg caggggtgg tgcgcttcct 360
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gcatggactc cacgtccatc agtacgggga ccttacaaac aactgcaaca gctgtgggaa 480
tcactttaac cctgatggag catctcatgg gggcccccag gactctgacc ggcaccgcgg 540
agacctgggc aatgtccgtg ctgatgctga cggccgcgcc atcttcagaa tggaggatga 600
gcagctgaag gtgtgggatg tgattggccg cagcctgatt attgatgagg gagaagatga 660
cctgggccgg ggaggccatc ccttatccaa gatcacaggg aactccgggg agaggttggc 720
ctgtggcatc attgcacgct ccgctggcct tttccagaac cccaagcaga tctgctcttg 780
cgatggcctc accatctggg aggagcgagg ccggcccatc gctggcaagg gcccgaaagg 840
agtcagcgca gcccctgccc acctttgagc agacctcact tggctctgtt gctgtcctcc 900
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<210> 21

<211> 288
<212> PRT
<213> Homo Sapien

<400> 21
Ala Gly Gly Val Leu Arg Leu Gly Val Val Thr Gly Ser Arg Met Ala
 1   5   10   15
Ser Asp Ser Gly Asn Gln Gly Thr Leu Cys Thr Leu Glu Phe Ala Val
            20   25   30
Gln Met Thr Cys Gln Ser Cys Val Asp Ala Val Arg Lys Ser Leu Gln
        35   40   45
Gly Val Ala Gly Val Gln Asp Val Glu Val His Leu Glu Asp Gln Met
    50   55   60
Val Leu Val His Thr Thr Leu Pro Ser Gln Glu Val Gln Ala Leu Leu
65   70   75   80
Glu Gly Thr Gly Arg Gln Ala Val Leu Lys Gly Met Gly Ser Gly Gln
                85   90   95
Leu Gln Asn Leu Gly Ala Ala Val Ala Ile Leu Gly Gly Pro Gly Thr
            100   105   110
Val Gln Gly Val Val Arg Phe Leu Gln Leu Thr Pro Glu Arg Cys Leu
        115   120   125
Ile Glu Gly Thr Ile Asp Gly Leu Glu Pro Gly Leu His Gly Leu His
    130   135   140
Val His Gln Tyr Gly Asp Leu Thr Asn Asn Cys Asn Ser Cys Gly Asn
145   150   155   160
His Phe Asn Pro Asp Gly Ala Ser His Gly Gly Pro Gln Asp Ser Asp
                165   170   175
Arg His Arg Gly Asp Leu Gly Asn Val Arg Ala Asp Ala Asp Gly Arg
            180   185   190
Ala Ile Phe Arg Met Glu Asp Glu Gln Leu Lys Val Trp Asp Val Ile
        195   200   205
Gly Arg Ser Leu Ile Ile Asp Glu Gly Glu Asp Asp Leu Gly Arg Gly
    210   215   220
Gly His Pro Leu Ser Lys Ile Thr Gly Asn Ser Gly Glu Arg Leu Ala
225   230   235   240
Cys Gly Ile Ile Ala Arg Ser Ala Gly Leu Phe Gln Asn Pro Lys Gln
                245   250   255
Ile Cys Ser Cys Asp Gly Leu Thr Ile Trp Glu Glu Arg Gly Arg Pro
            260   265   270
Ile Ala Gly Lys Gly Pro Lys Gly Val Ser Ala Ala Pro Ala His Leu
        275   280   285

<210> 22
<211> 1006
<212> DNA
<213> Homo Sapien

<400> 22
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ttaagcgatg cctttgccca ggtgaacccc ctcaagaagg tgccagcctt gaaggacggg 180
gacttcacct tgacggagag tgtggccatc ctgctctacc tgacgcgcaa atataaggtc 240
cctgactact ggtaccctca ggacctgcag gcccgtgccc gtgtggatga gtacctggca 300
tggcagcaca cgactctgcg gagaagctgc ctccgggcct tgtggcataa ggtgatgttc 360
cctgttttcc tgggtgagcc agtatctccc cagacactgg cagccaccct ggcagagttg 420

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gcagtggggg aggacctctt ccaggaggcc catgaggtca ttctgaaggc caaggacttc     660
ccacctgcag accccaccat aaagcagaag ctgatgccct gggtgctggc catgatccgg     720
tgagctggga aacctcaccc ttgcaccgtc ctcagcagtc cacaaagcat tttcatttct     780
aatggcccat gggagccagg cccagaaagc aggaatggct tgcttaagac ttgcccaagt     840
cccagagcac ctcacctccc gaagccacca tccccaccct gtcttccaca gccgcctgaa     900
agccacaatg agaatgatgc acactgaggc cttgtgtccc tttaatcact gcatttcatt     960
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<210> 23
<211> 240
<212> PRT
<213> Homo Sapien

<400> 23
Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
 1               5                  10                  15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
            20                  25                  30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
        35                  40                  45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
    50                  55                  60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65                  70                  75                  80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp
                85                  90                  95
Glu Tyr Leu Ala Trp Gln His Thr Thr Leu Arg Arg Ser Cys Leu Arg
            100                 105                 110
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Glu Pro Val
        115                 120                 125
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu
    130                 135                 140
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly
145                 150                 155                 160
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His
                165                 170                 175
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala
            180                 185                 190
Thr Trp Arg Gln Arg Val Glu Ala Ala Val Gly Glu Asp Leu Phe Gln
        195                 200                 205
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp
    210                 215                 220
Pro Thr Ile Lys Gln Lys Leu Met Pro Trp Val Leu Ala Met Ile Arg
225                 230                 235                 240

<210> 24
<211> 2442
<212> DNA
<213> Homo Sapien

<400> 24
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gacacagatg gcaaaggtat cctgaacaaa caagaattct ttgttgcttt gcgtcttgtg 240
gcatgtgccc agaatggatt ggaagtttca ctaagtagtt tgaacctggc tgttcctcca 300
ccaagatttc ctgaagataa ggccaaatat gatgcaatat ttgatagttt aagcccagtg 360
aatggatttc tgtctggtga taaagtgaaa ccagtgttgc tcaactctaa gttacctgtg 420
gatatccttg gaagagtttg ggagttgagt gatattgacc atgatggaat gcttgacaga 480
gatgagtttg cagttgccat gtttttggta tactgtgcac tggagaaaga acctgtgcca 540
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tctgtgcggt tgatcccctc ttcagcatca gccaaggaat cttaccactc cttaccatct 660
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ctggctattg cactcagcaa atctgagata tcagaagcat ga 2442

<210> 25
<211> 813
<212> PRT
<213> Homo Sapien

<400> 25
Met Ala Ala Ala Ala Gln Leu Ser Leu Thr Gln Leu Ser Ser Gly Asn
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Pro Val Tyr Glu Lys Tyr Tyr Arg Gln Val Asp Thr Gly Asn Thr Gly
            20   25   30
Arg Val Leu Ala Ser Asp Ala Ala Ala Phe Leu Lys Lys Ser Gly Leu
        35   40   45
Pro Asp Leu Ile Leu Gly Lys Ile Trp Asp Leu Ala Asp Thr Asp Gly
    50   55   60

Lys Gly Ile Leu Asn Lys Gln Glu Phe Phe Val Ala Leu Arg Leu Val
65 70 75 80
Ala Cys Ala Gln Asn Gly Leu Glu Val Ser Leu Ser Ser Leu Asn Leu
85 90 95
Ala Val Pro Pro Pro Arg Phe Pro Glu Asp Lys Ala Lys Tyr Asp Ala
100 105 110
Ile Phe Asp Ser Leu Ser Pro Val Asn Gly Phe Leu Ser Gly Asp Lys
115 120 125
Val Lys Pro Val Leu Leu Asn Ser Lys Leu Pro Val Asp Ile Leu Gly
130 135 140
Arg Val Trp Glu Leu Ser Asp Ile Asp His Asp Gly Met Leu Asp Arg
145 150 155 160
Asp Glu Phe Ala Val Ala Met Phe Leu Val Tyr Cys Ala Leu Glu Lys
165 170 175
Glu Pro Val Pro Met Ser Leu Pro Pro Ala Leu Val Pro Pro Ser Lys
180 185 190
Arg Lys Thr Val Ser Ile Ser Gly Ser Val Arg Leu Ile Pro Ser Ser
195 200 205
Ala Ser Ala Lys Glu Ser Tyr His Ser Leu Pro Ser Val Gly Ile Leu
210 215 220
Pro Thr Lys Ala Pro Leu Arg Gln Trp Val Val Ser Pro Ala Glu Lys
225 230 235 240
Ala Lys Tyr Asp Glu Ile Phe Leu Lys Thr Asp Lys Asp Met Asp Gly
245 250 255
Phe Val Ser Gly Leu Glu Val Arg Glu Ile Phe Leu Lys Thr Gly Leu
260 265 270
Pro Ser Thr Leu Leu Ala His Ile Trp Ser Leu Cys Asp Thr Lys Asp
275 280 285
Cys Gly Lys Leu Ser Lys Asp Gln Phe Ala Leu Ala Phe His Leu Ile
290 295 300
Ser Gln Lys Leu Ile Lys Gly Ile Asp Pro Pro His Val Leu Thr Pro
305 310 315 320
Glu Met Ile Pro Pro Ser Asp Arg Ala Ser Leu Gln Lys Asn Ile Ile
325 330 335
Gly Ser Ser Pro Val Ala Asp Phe Ser Ala Ile Lys Glu Leu Asp Thr
340 345 350
Leu Asn Asn Glu Ile Val Asp Leu Gln Arg Glu Lys Asn Asn Val Glu
355 360 365
Gln Asp Leu Lys Glu Lys Glu Asp Thr Ile Lys Gln Arg Thr Ser Glu
370 375 380
Val Gln Asp Leu Gln Asp Glu Val Gln Arg Glu Asn Thr Asn Leu Gln
385 390 395 400
Lys Leu Gln Ala Gln Lys Gln Gln Val Gln Glu Leu Leu Asp Glu Leu
405 410 415
Asp Glu Gln Lys Ala Gln Leu Glu Glu Gln Leu Lys Glu Val Arg Lys
420 425 430
Lys Cys Ala Glu Glu Ala Gln Leu Ile Ser Ser Leu Lys Ala Glu Leu
435 440 445
Thr Ser Gln Glu Ser Gln Ile Ser Thr Tyr Glu Glu Glu Leu Ala Lys
450 455 460
Ala Arg Glu Glu Leu Ser Arg Leu Gln Gln Glu Thr Ala Glu Leu Glu
465 470 475 480
Glu Ser Val Glu Ser Gly Lys Ala Gln Leu Glu Pro Leu Gln Gln His
485 490 495
Leu Gln Asp Ser Gln Gln Glu Ile Ser Ser Met Gln Met Lys Leu Met

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            500                 505                 510
Glu Met Lys Asp Leu Glu Asn His Asn Ser Gln Leu Asn Trp Cys Ser
        515                 520                 525
Ser Pro His Ser Ile Leu Val Asn Gly Ala Thr Asp Tyr Cys Ser Leu
    530                 535                 540
Ser Thr Ser Ser Ser Glu Thr Ala Asn Leu Asn Glu His Val Glu Gly
545                 550                 555                 560
Gln Ser Asn Leu Glu Ser Glu Pro Ile His Gln Glu Ser Pro Ser Asp
                565                 570                 575
Pro Phe Val Gly Asn Pro Phe Gly Gly Asp Pro Phe Lys Gly Ser Asp
            580                 585                 590
Pro Phe Ala Ser Asp Cys Phe Phe Arg Gln Ser Thr Asp Pro Phe Ala
        595                 600                 605
Thr Ser Ser Thr Asp Pro Phe Ser Ala Ala Asn Asn Ser Ser Ile Thr
    610                 615                 620
Ser Val Glu Thr Leu Lys His Asn Asp Pro Phe Ala Pro Gly Gly Thr
625                 630                 635                 640
Val Val Ala Ala Ser Asp Ser Ala Thr Asp Pro Phe Ala Ser Val Phe
                645                 650                 655
Gly Asn Glu Ser Phe Gly Gly Gly Phe Ala Asp Phe Ser Thr Leu Ser
            660                 665                 670
Lys Val Asn Asn Glu Asp Pro Phe Arg Ser Ala Thr Ser Ser Ser Val
        675                 680                 685
Ser Asn Val Val Ile Thr Lys Asn Val Phe Glu Glu Thr Ser Val Lys
    690                 695                 700
Ser Glu Asp Glu Pro Pro Ala Leu Pro Pro Lys Ile Gly Thr Pro Thr
705                 710                 715                 720
Arg Pro Cys Pro Leu Pro Pro Gly Asn Asp Ser Pro Lys Glu Lys Asp
                725                 730                 735
Pro Glu Met Phe Cys Asp Pro Phe Thr Ser Ala Thr Thr Thr Thr Asn
            740                 745                 750
Lys Glu Ala Asp Pro Ser Asn Phe Ala Asn Phe Ser Ala Tyr Pro Ser
        755                 760                 765
Glu Glu Asp Met Ile Glu Trp Ala Lys Arg Glu Ser Glu Arg Glu Glu
    770                 775                 780
Glu Gln Arg Leu Ala Arg Leu Asn Gln Gln Glu Gln Glu Asp Leu Glu
785                 790                 795                 800
Leu Ala Ile Ala Leu Ser Lys Ser Glu Ile Ser Glu Ala
                805                 810
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<210> 26
<211> 1357
<212> DNA
<213> Homo Sapien

<400> 26

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cagatccgca cggtaattca gtaccaaact gttcgatatg atatcctccc cttatctcct     180
gtgtcccgga atcggctagc ccaggtgaag aggaagatcc tggtgctgga tctggatgag     240
acacttattc actcccacca tgatggggtc ctgaggccca cagtccggcc tggtacgcct     300
cctgacttca tcctcaaggt ggtaatagac aaacatcctg tccggttttt tgtacataag     360
aggccccatg tggatttctt cctggaagtg gtgagccagt ggtacgagct ggtggtgttt     420
acagcaagca tggagatcta tggctctgct gtggcagata aactggacaa tagcagaagc     480
attcttaaga ggagatatta cagacagcac tgcactttgg agttgggcag ctacatcaag     540
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gacctctctg tggtccacag tgacctctcc agcattgtga tcctggataa ctccccaggg     600
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gacacagccc ttctcaacct gctcccaatg ctggatgccc tcaggttcac cgctgatgtt     720
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gccctacact ccacttggga gtctggatgg acacatgggc caggggctct gaagcagcct     960
cactcttaac ttcgtgttca cactccatgg aaaccccaga ctgggacaca ggcggaagcc    1020
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<210> 27
<211> 254
<212> PRT
<213> Homo Sapien

<400> 27

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Leu Leu Gly Leu Arg Thr Phe Val Ala Phe Ala Ala Lys Leu Trp Ser
            20                  25                  30
Phe Phe Ile Tyr Leu Leu Arg Arg Gln Ile Arg Thr Val Ile Gln Tyr
        35                  40                  45
Gln Thr Val Arg Tyr Asp Ile Leu Pro Leu Ser Pro Val Ser Arg Asn
    50                  55                  60
Arg Leu Ala Gln Val Lys Arg Lys Ile Leu Val Leu Asp Leu Asp Glu
65                  70                  75                  80
Thr Leu Ile His Ser His His Asp Gly Val Leu Arg Pro Thr Val Arg
                85                  90                  95
Pro Gly Thr Pro Pro Asp Phe Ile Leu Lys Val Val Ile Asp Lys His
            100                 105                 110
Pro Val Arg Phe Phe Val His Lys Arg Pro His Val Asp Phe Phe Leu
        115                 120                 125
Glu Val Val Ser Gln Trp Tyr Glu Leu Val Val Phe Thr Ala Ser Met
    130                 135                 140
Glu Ile Tyr Gly Ser Ala Val Ala Asp Lys Leu Asp Asn Ser Arg Ser
145                 150                 155                 160
Ile Leu Lys Arg Arg Tyr Tyr Arg Gln His Cys Thr Leu Glu Leu Gly
                165                 170                 175
Ser Tyr Ile Lys Asp Leu Ser Val Val His Ser Asp Leu Ser Ser Ile
            180                 185                 190
Val Ile Leu Asp Asn Ser Pro Gly Ala Tyr Arg Ser His Pro Asp Asn
        195                 200                 205
Ala Ile Pro Ile Lys Ser Trp Phe Ser Asp Pro Ser Asp Thr Ala Leu
    210                 215                 220
Leu Asn Leu Leu Pro Met Leu Asp Ala Leu Arg Phe Thr Ala Asp Val
225                 230                 235                 240
Arg Ser Val Leu Ser Arg Asn Leu His Gln His Arg Leu Trp
                245                 250
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<210> 28

<211> 1812
<212> DNA
<213> Homo Sapien

<400> 28
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aaatttgcag agcatggagg ttggcacgtt tatggccttc ttcagaggtc agacaagaag 180
tatgatgaag ccattaagtg ttacagaaat gcactaaaat gggataaaga caatcttcaa 240
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gaggaagcct ggactaaata tcccagggga ctggtgccaa gaaggctgcc gttaaacttt 660
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aatgaaattt ga 1812

<210> 29
<211> 603
<212> PRT
<213> Homo Sapien

<400> 29
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Cys Lys Gln Ile Leu Ser Asn Pro Lys Phe Ala Glu His Gly Gly Trp
        35   40   45
His Val Tyr Gly Leu Leu Gln Arg Ser Asp Lys Lys Tyr Asp Glu Ala
    50   55   60
Ile Lys Cys Tyr Arg Asn Ala Leu Lys Trp Asp Lys Asp Asn Leu Gln
65   70   75   80
Ile Leu Arg Asp Leu Ser Leu Leu Gln Ile Gln Met Arg Asp Leu Glu
                85   90   95

Gly Tyr Arg Thr Ser Pro Asp Lys Val Asp Tyr Glu Tyr Ser Glu Leu
100 105 110
Leu Leu Tyr Gln Asn Gln Val Leu Arg Glu Ala Gly Leu Tyr Arg Glu
115 120 125
Ala Leu Glu His Leu Cys Thr Tyr Glu Lys Gln Ile Cys Asp Lys Leu
130 135 140
Ala Val Glu Glu Thr Lys Gly Glu Leu Leu Leu Gln Leu Cys Arg Leu
145 150 155 160
Glu Asp Ala Ala Asp Val Tyr Arg Gly Leu Gln Glu Arg Asn Pro Glu
165 170 175
Asn Trp Ala Tyr Tyr Lys Gly Leu Glu Lys Ala Leu Lys Pro Ala Asn
180 185 190
Met Leu Glu Arg Leu Lys Ile Tyr Glu Glu Ala Trp Thr Lys Tyr Pro
195 200 205
Arg Gly Leu Val Pro Arg Arg Leu Pro Leu Asn Phe Leu Ser Gly Glu
210 215 220
Lys Phe Lys Glu Cys Leu Asp Lys Phe Leu Arg Met Asn Phe Ser Lys
225 230 235 240
Gly Cys Pro Pro Val Phe Asn Thr Leu Arg Ser Leu Tyr Lys Asp Lys
245 250 255
Glu Lys Val Ala Ile Ile Glu Glu Leu Val Val Gly Tyr Glu Thr Ser
260 265 270
Leu Lys Ser Cys Arg Leu Phe Asn Pro Asn Asp Asp Gly Lys Glu Glu
275 280 285
Pro Pro Thr Thr Leu Leu Trp Val Gln Tyr Tyr Leu Ala Gln His Tyr
290 295 300
Asp Lys Ile Gly Gln Pro Ser Ile Ala Leu Glu Tyr Ile Asn Thr Ala
305 310 315 320
Ile Glu Ser Thr Pro Thr Leu Ile Glu Leu Phe Leu Val Lys Ala Lys
325 330 335
Ile Tyr Lys His Ala Gly Asn Ile Lys Glu Ala Ala Arg Trp Met Asp
340 345 350
Glu Ala Gln Ala Leu Asp Thr Ala Asp Arg Phe Ile Asn Ser Lys Cys
355 360 365
Ala Lys Tyr Met Leu Lys Ala Asn Leu Ile Lys Glu Ala Glu Glu Met
370 375 380
Cys Ser Lys Phe Thr Arg Glu Gly Thr Ser Ala Val Glu Asn Leu Asn
385 390 395 400
Glu Met Gln Cys Met Trp Phe Gln Thr Glu Cys Ala Gln Ala Tyr Lys
405 410 415
Ala Met Asn Lys Phe Gly Glu Ala Leu Lys Lys Cys His Glu Ile Glu
420 425 430
Arg His Phe Ile Glu Ile Thr Asp Asp Gln Phe Asp Phe His Thr Tyr
435 440 445
Cys Met Arg Lys Ile Thr Leu Arg Ser Tyr Val Asp Leu Leu Lys Leu
450 455 460
Glu Asp Val Leu Arg Gln His Pro Phe Tyr Phe Lys Ala Ala Arg Ile
465 470 475 480
Ala Ile Glu Ile Tyr Leu Lys Leu His Asp Asn Pro Leu Thr Asp Glu
485 490 495
Asn Lys Glu His Glu Ala Asp Thr Ala Ala Lys Met Val Tyr Tyr Leu
500 505 510
Asp Pro Ser Ser Gln Lys Arg Ala Ile Glu Leu Ala Thr Thr Leu Asp
515 520 525
Glu Ser Leu Thr Asn Arg Asn Leu Gln Thr Cys Met Glu Val Leu Glu

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    530                 535                 540
Ala Leu Tyr Asp Gly Ser Leu Gly Asp Cys Lys Glu Ala Ala Glu Ile
545                 550                 555                 560
Tyr Arg Ala Asn Cys His Lys Leu Phe Pro Tyr Ala Leu Ala Phe Met
                565                 570                 575
Pro Pro Gly Tyr Glu Glu Asp Met Lys Ile Thr Val Asn Gly Asp Ser
            580                 585                 590
Ser Ala Glu Ala Glu Glu Leu Ala Asn Glu Ile
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<210> 30
<211> 1351
<212> DNA
<213> Homo Sapien

<400> 30

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gcaaacgtga ccgttgatcc agatgaagaa atggccaaaa tcgacaggac ggcgagggac     180
cagtgtggga gccagccttg ggacaataat gcagtctgtg cagacccctg ctccctgatc     240
cccacacctg acaaagaaga tgatgaccgg gtttacccaa actcaacgtg caagcctcgg     300
attattgcac catccagagg ctccccgctg cctgtactga gctgggcaaa tagagaggaa     360
gtctggaaaa tcatgttaaa caaggaaaag acatacttaa gggatcagca ctttcttgag     420
caacaccctc ttctgcagcc aaaaatgcga gcaattcttc tggattggtt aatggaggtg     480
tgtgaagtct ataaacttca cagggagacc ttttacttgg cacaagattt ctttgaccgg     540
tatatggcga cacaagaaaa tgttgtaaaa actcttttac agcttattgg gatttcatct     600
ttatttattg cagccaaact tgaggaaatc tatcctccaa agttgcacca gtttgcgtat     660
gtgacagatg gagcttgttc aggagatgaa attctcacca tggaattaat gattatgaag     720
gcccttaagt ggcgtttaag tcccctgact attgtgtcct ggctgaatgt atacatgcag     780
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gtttcagggt atcagtggtg cgacatagag aactgtgtca agtggatggt tccatttgcc    1020
atggttataa gggagacggg gagctcaaaa ctgaagcact tcaggggcgt cgctgatgaa    1080
gatgcacaca acatacagac ccacagagac agcttggatt tgctggacaa agcccgagca    1140
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<211> 451
<212> PRT
<213> Homo Sapien

<220>
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<400> 31

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            20                  25                  30
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Glu Glu Met Ala Lys Ile Asp Arg Thr Ala Arg Asp Gln Cys Gly Ser
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Gln Pro Trp Asp Asn Asn Ala Val Cys Ala Asp Pro Cys Ser Leu Ile
65 70 75 80
Pro Thr Pro Asp Lys Glu Asp Asp Asp Arg Val Tyr Pro Asn Ser Thr
85 90 95
Cys Lys Pro Arg Ile Ile Ala Pro Ser Arg Gly Ser Pro Leu Pro Val
100 105 110
Leu Ser Trp Ala Asn Arg Glu Glu Val Trp Lys Ile Met Leu Asn Lys
115 120 125
Glu Lys Thr Tyr Leu Arg Asp Gln His Phe Leu Glu Gln His Pro Leu
130 135 140
Leu Gln Pro Lys Met Arg Ala Ile Leu Leu Asp Trp Leu Met Glu Val
145 150 155 160
Cys Glu Val Tyr Lys Leu His Arg Glu Thr Phe Tyr Leu Ala Gln Asp
165 170 175
Phe Phe Asp Arg Tyr Met Ala Thr Gln Glu Asn Val Val Lys Thr Leu
180 185 190
Leu Gln Leu Ile Gly Ile Ser Ser Leu Phe Ile Ala Ala Lys Leu Glu
195 200 205
Glu Ile Tyr Pro Pro Lys Leu His Gln Phe Ala Tyr Val Thr Asp Gly
210 215 220
Ala Cys Ser Gly Asp Glu Ile Leu Thr Met Glu Leu Met Ile Met Lys
225 230 235 240
Ala Leu Lys Trp Arg Leu Ser Pro Leu Thr Ile Val Ser Trp Leu Asn
245 250 255
Val Tyr Met Gln Val Ala Tyr Leu Asn Asp Leu His Glu Val Leu Leu
260 265 270
Pro Gln Tyr Pro Gln Gln Ile Phe Ile Gln Ile Ala Glu Leu Leu Asp
275 280 285
Leu Cys Val Leu Asp Val Asp Cys Leu Glu Phe Pro Tyr Gly Ile Leu
290 295 300
Ala Ala Ser Ala Leu Tyr His Phe Ser Ser Ser Glu Leu Met Gln Lys
305 310 315 320
Val Ser Gly Tyr Gln Trp Cys Asp Ile Glu Asn Cys Val Lys Trp Met
325 330 335
Val Pro Phe Ala Met Val Ile Arg Glu Thr Gly Ser Ser Lys Leu Lys
340 345 350
His Phe Arg Gly Val Ala Asp Glu Asp Ala His Asn Ile Gln Thr His
355 360 365
Arg Asp Ser Leu Asp Leu Leu Asp Lys Ala Arg Ala Lys Lys Ala Met
370 375 380
Leu Ser Glu Gln Asn Arg Ala Ser Pro Leu Pro Ser Gly Leu Leu Thr
385 390 395 400
Pro Pro Gln Ser Gly Val Leu Gly Ser Val Val Pro Ser Gly Ala Gly
405 410 415
Gly Cys Gly Gln Ala Leu Cys Arg Ala His Ser Gln Leu Gly Arg Gly
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Leu Thr Ser Pro His Tyr Gln Leu Thr Val Tyr Asn Ala Phe Asp Glu
435 440 445
Leu Phe Xaa
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<210> 32
<211> 3750
<212> DNA
<213> Homo Sapien

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gttggctctc ctgtaggaag caaccagtct cgatctggcc caatctctcc tgcaagtatc    240
ccaggtttta tggcaggcac acaaagaaac cctcagatgg ctcagtatgg acctcaacag    300
acaggaccat ccatgtcgcc tcatccttct cctgggggcc agatgcatgc tggaatcagt    360
agctttcagc agagtaactc aagtgggact tacggtccac agatgagcca gtatggacca    420
caaggtaact actccagacc cccagcgtat agtggggtgc ccagtgcaag ctacagcggc    480
ccagggcccg gtatgggtat cagtgccaac aaccagatgc atggacaagg gccaagccag    540
ccatgtggtg ctgtgcccct gggacgaatg ccatcagctg ggatgcagaa cagaccattt    600
cctggaaata tgagcagcat gacccccagt tctcctggca tgtctcagca gggagggcca    660
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gccagttacg accgaagcac tgttgctact ttcaatctct cccagttgtc tggatttctc   2040
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gaccgatctg acaagttggg gcgtgtgcag gagttcaata gtggccttct gcactggcag   2460
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<210> 33
<211> 1249
<212> PRT
<213> Homo Sapien

<400> 33
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Gln Ser Asn Pro Ala Gln Ser Pro Phe Ser Pro His Ala Ser Pro His
35 40 45
Leu Ser Ser Ile Pro Gly Gly Pro Ser Pro Ser Pro Val Gly Ser Pro
50 55 60
Val Gly Ser Asn Gln Ser Arg Ser Gly Pro Ile Ser Pro Ala Ser Ile
65 70 75 80
Pro Gly Phe Met Ala Gly Thr Gln Arg Asn Pro Gln Met Ala Gln Tyr
85 90 95
Gly Pro Gln Gln Thr Gly Pro Ser Met Ser Pro His Pro Ser Pro Gly
100 105 110
Gly Gln Met His Ala Gly Ile Ser Ser Phe Gln Gln Ser Asn Ser Ser
115 120 125
Gly Thr Tyr Gly Pro Gln Met Ser Gln Tyr Gly Pro Gln Gly Asn Tyr
130 135 140
Ser Arg Pro Pro Ala Tyr Ser Gly Val Pro Ser Ala Ser Tyr Ser Gly
145 150 155 160
Pro Gly Pro Gly Met Gly Ile Ser Ala Asn Asn Gln Met His Gly Gln
165 170 175
Gly Pro Ser Gln Pro Cys Gly Ala Val Pro Leu Gly Arg Met Pro Ser
180 185 190
Ala Gly Met Gln Asn Arg Pro Phe Pro Gly Asn Met Ser Ser Met Thr
195 200 205
Pro Ser Ser Pro Gly Met Ser Gln Gln Gly Gly Pro Gly Met Gly Pro
210 215 220
Pro Met Pro Thr Val Asn Arg Lys Ala Gln Glu Ala Ala Ala Ala Val
225 230 235 240
Met Gln Ala Ala Ala Asn Ser Ala Gln Ser Arg Tyr Ala Thr Gln Glu
245 250 255
His Ala Pro Gly Arg Gln Gly Ser Phe Pro Gly Met Asn Gln Ser Gly
260 265 270

Leu Met Ala Ser Ser Ser Pro Tyr Ser Gln Pro Met Asn Asn Ser Ser
275 280 285
Ser Leu Met Asn Thr Gln Ala Pro Pro Tyr Ser Met Ala Pro Ala Met
290 295 300
Val Asn Ser Ser Ala Ala Ser Val Gly Leu Ala Asp Met Met Ser Pro
305 310 315 320
Gly Glu Ser Lys Leu Pro Leu Pro Leu Lys Ala Asp Gly Lys Glu Glu
325 330 335
Gly Thr Pro Gln Pro Glu Ser Lys Ser Lys Asp Ser Tyr Ser Ser Gln
340 345 350
Gly Ile Ser Gln Pro Pro Thr Pro Gly Asn Leu Pro Val Pro Ser Pro
355 360 365
Met Ser Pro Ser Ser Ala Ser Ile Ser Ser Phe His Gly Asp Glu Ser
370 375 380
Asp Ser Ile Ser Ser Pro Gly Trp Pro Lys Thr Pro Ser Ser Pro Lys
385 390 395 400
Ser Ser Ser Ser Thr Thr Thr Gly Glu Lys Ile Thr Lys Val Tyr Glu
405 410 415
Leu Gly Asn Glu Pro Glu Arg Lys Leu Trp Val Asp Arg Tyr Leu Thr
420 425 430
Phe Met Glu Glu Arg Gly Ser Pro Val Ser Ser Leu Pro Ala Val Gly
435 440 445
Lys Lys Pro Leu Asp Leu Phe Arg Leu Tyr Val Cys Val Lys Glu Ile
450 455 460
Gly Gly Leu Ala Gln Val Asn Lys Asn Lys Lys Trp Arg Glu Leu Ala
465 470 475 480
Thr Asn Leu Asn Val Gly Thr Ser Ser Ser Ala Ala Ser Ser Met Lys
485 490 495
Lys Gln Tyr Ile Gln Tyr Leu Phe Ala Phe Glu Ser Lys Ile Glu Pro
500 505 510
Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln Ser Thr Gly Ser
515 520 525
Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro Pro Thr Pro Ala
530 535 540
Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly Gly Arg Ser Ser
545 550 555 560
Thr Ile Ser Val His Asp Pro Phe Ser Asp Val Ser Asp Ser Ser Phe
565 570 575
Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr Gln Gln Gly Met
580 585 590
Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu Pro Asn Lys Asp
595 600 605
Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser Glu Pro Phe Met
610 615 620
Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp Met Tyr Asn Gln
625 630 635 640
Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly Gln Arg Gln Gln
645 650 655
Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Ser Thr Val Ala Thr Phe Asn
660 665 670
Leu Ser Gln Leu Ser Gly Phe Leu Glu Leu Leu Val Glu Tyr Phe Arg
675 680 685
Lys Cys Leu Ile Asp Ile Phe Gly Ile Leu Met Glu Tyr Glu Val Gly
690 695 700
Asp Pro Ser Gln Lys Ala Leu Asp His Asn Ala Ala Arg Lys Asp Asp

705 710 715 720
Ser Gln Ser Leu Ala Asp Asp Ser Gly Lys Glu Glu Glu Asp Ala Glu
725 730 735
Cys Ile Asp Asp Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Ser
740 745 750
Glu Lys Thr Glu Ser Asp Glu Lys Ser Ser Ile Ala Leu Thr Ala Pro
755 760 765
Asp Ala Ala Ala Asp Pro Lys Glu Lys Pro Lys Gln Ala Ser Lys Phe
770 775 780
Asp Lys Leu Pro Ile Lys Ile Val Lys Lys Asn Asn Leu Phe Val Val
785 790 795 800
Asp Arg Ser Asp Lys Leu Gly Arg Val Gln Glu Phe Asn Ser Gly Leu
805 810 815
Leu His Trp Gln Leu Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr
820 825 830
His Phe Glu Ser Lys Met Glu Ile Pro Pro Arg Arg Arg Pro Pro Pro
835 840 845
Pro Leu Ser Ser Ala Gly Arg Lys Lys Glu Gln Glu Gly Lys Gly Asp
850 855 860
Ser Glu Glu Gln Gln Glu Lys Ser Ile Ile Ala Thr Ile Asp Asp Val
865 870 875 880
Leu Ser Ala Arg Pro Gly Ala Leu Pro Glu Asp Ala Asn Pro Gly Pro
885 890 895
Gln Thr Glu Ser Ser Lys Phe Pro Phe Gly Ile Gln Gln Ala Lys Ser
900 905 910
His Arg Asn Ile Lys Leu Leu Glu Asp Glu Pro Arg Ser Arg Asp Glu
915 920 925
Thr Pro Leu Cys Thr Ile Ala His Trp Gln Asp Ser Leu Ala Lys Arg
930 935 940
Cys Ile Cys Val Ser Asn Ile Val Arg Ser Leu Ser Phe Val Pro Gly
945 950 955 960
Asn Asp Ala Glu Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly
965 970 975
Lys Leu Ile Leu Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro
980 985 990
Gln Thr Tyr Glu Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser
995 1000 1005
Lys Asp Glu Trp Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr
1010 1015 1020
Leu Val Thr Leu Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr
1025 1030 1035 1040
Thr Glu Ser Ile Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met
1045 1050 1055
Val Cys Pro Ser Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro
1060 1065 1070
Asn Ser Val Leu Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys
1075 1080 1085
Leu Ser Ile Gln Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro
1090 1095 1100
Phe Ser Arg Gln Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly
1105 1110 1115 1120
Asp Arg Lys Asn Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser
1125 1130 1135
Asn Leu Ala Gln Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln
1140 1145 1150

Lys Gly Ser Ile Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr
1155 1160 1165
Met Ala Gln Tyr Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro
1170 1175 1180
Pro Pro Leu Glu Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys
1185 1190 1195 1200
Ala Leu Leu Ala Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu
1205 1210 1215
Leu His Glu Gly Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn
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Ser Leu Val Ala Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln
1235 1240 1245
Leu

<210> 34
<211> 2887
<212> DNA
<213> Homo Sapien

<400> 34
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aagtatattt ttgtatgctt tgttttgtga cttaaaagtg ttacctttgt agtcaaattt 2820
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<210> 35
<211> 488
<212> PRT
<213> Homo Sapien

<400> 35
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Lys Ala Val Asp Lys Ile Pro Val Thr Leu Ser Gly Phe Val His Gln
            20   25   30
Leu Ser Asp Asn Ile Tyr Pro Val Glu Asp Leu Ala Ala Thr Ser Val
        35   40   45
Thr Ile Phe Pro Asn Ala Glu Leu Gly Gly Pro Phe Asp Gln Met Asn
    50   55   60
Gly Val Ala Gly Asp Gly Met Ile Asn Ile Asp Met Thr Gly Glu Lys
65   70   75   80
Arg Ser Leu Asp Leu Pro Tyr Pro Ser Ser Phe Ala Pro Val Ser Ala
                85   90   95
Pro Arg Asn Gln Thr Phe Thr Tyr Met Gly Lys Phe Ser Ile Asp Pro
            100   105   110
Gln Tyr Pro Gly Ala Ser Cys Tyr Pro Glu Gly Ile Ile Asn Ile Val
        115   120   125
Ser Ala Gly Ile Leu Gln Gly Val Thr Ser Pro Ala Ser Thr Thr Ala
    130   135   140
Ser Ser Ser Val Thr Ser Ala Ser Pro Asn Pro Leu Ala Thr Gly Pro
145   150   155   160
Leu Gly Val Cys Thr Met Ser Gln Thr Gln Pro Asp Leu Asp His Leu
                165   170   175
Tyr Ser Pro Pro Pro Pro Pro Pro Pro Tyr Ser Gly Cys Ala Gly Asp
            180   185   190
Leu Tyr Gln Asp Pro Ser Ala Phe Leu Ser Ala Ala Thr Thr Ser Thr
        195   200   205
Ser Ser Ser Leu Ala Tyr Pro Pro Pro Pro Ser Tyr Pro Ser Pro Lys
    210   215   220
Pro Ala Thr Asp Pro Gly Leu Phe Pro Met Ile Pro Asp Tyr Pro Gly
225   230   235   240
Phe Phe Pro Ser Gln Cys Gln Arg Asp Leu His Gly Thr Ala Gly Pro
                245   250   255
Asp Arg Lys Pro Phe Pro Cys Pro Leu Asp Thr Leu Arg Val Pro Pro

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            260                 265                 270
Pro Leu Thr Pro Leu Ser Thr Ile Arg Asn Phe Thr Leu Gly Gly Pro
        275                 280                 285
Ser Ala Gly Val Thr Gly Pro Gly Ala Ser Gly Gly Ser Glu Gly Pro
    290                 295                 300
Arg Leu Pro Gly Ser Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala
305                 310                 315                 320
Ala Tyr Asn Pro His His Leu Pro Leu Arg Pro Ile Leu Arg Pro Arg
                325                 330                 335
Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Val His Glu Arg Pro Tyr
            340                 345                 350
Pro Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu
        355                 360                 365
Leu Thr Arg His Ile Arg Ile His Thr Gly His Lys Pro Phe Gln Cys
    370                 375                 380
Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His
385                 390                 395                 400
Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Tyr Cys Gly
                405                 410                 415
Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His
            420                 425                 430
Leu Arg Gln Lys Glu Arg Lys Ser Ser Ala Pro Ser Ala Ser Val Pro
        435                 440                 445
Ala Pro Ser Thr Ala Ser Cys Ser Gly Gly Val Gln Pro Gly Gly Thr
    450                 455                 460
Leu Cys Ser Ser Asn Ser Ser Ser Leu Gly Gly Gly Pro Leu Ala Pro
465                 470                 475                 480
Cys Ser Ser Arg Thr Arg Thr Pro
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<210> 36
<211> 300
<212> DNA
<213> Homo Sapien

<400> 36
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ggcagtgggt acttcgatgt gagggacaag gaggaccagt ggatccggat cttcatggag 120
aagggagaca tggtgacgct ccccgcgggg atctatcacc gcttcacggt ggacgagaag 180
aactacacga aggccatgcg gctgtttgtg ggagaaccgg tgtggacagc gtacaaccgg 240
cccgctgacc attttgaagc ccgcgggcag tacgtgaaat ttctggcaca gaccgcctag 300

<210> 37
<211> 99
<212> PRT
<213> Homo Sapien

<400> 37
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Ile Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg
 1               5                  10                  15
Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp
            20                  25                  30
Gln Trp Ile Arg Ile Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro
        35                  40                  45
Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys
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50 55 60

Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg
65 70 75 80

Pro Ala Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala
85 90 95

Gln Thr Ala

<210> 38
<211> 2404
<212> DNA
<213> Homo Sapien

<400> 38

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ttaaaaactt ttgctaattt tccaagtggt agtcctgttt cagcatcaac actggcacga 180
gcagggtttc tttatactgg tgaaggagat accgtgcggt gctttagttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
tgcagattta tcaacggctt ttatcttgaa aatagtgcca cgcagtctac aaattctggt 360
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgcagactat cttttgagaa ctgggcaggt tgtagatata 480
tcagacacca tatacccgag gaaccctgcc atgtatagtg aagaagctag attaaagtcc 540
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
tgggaacctt gtgatcgtgc ctggtcagta acacaggcga cactttccta attgcttctt 720
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tgta 2404

<210> 39
<211> 278
<212> PRT
<213> Homo Sapien

<400> 39
His Arg Arg His Phe Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Leu
 1   5   10   15
Asn Ile Arg Ser Glu Ser Asp Ala Val Ser Ser Asp Arg Asn Phe Pro
            20   25   30
Asn Ser Thr Asn Leu Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala
        35   40   45
Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln
    50   55   60
Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys
65   70   75   80
Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp
                85   90   95
Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu
            100   105   110
Glu Gln Lys Gly Gln Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser
        115   120   125
Leu Glu Glu Cys Leu Val Arg Thr Thr Glu Lys Thr Pro Ser Leu Thr
    130   135   140
Arg Arg Ile Asp Asp Thr Ile Phe Gln Asn Pro Met Val Gln Glu Ala
145   150   155   160
Ile Arg Met Gly Phe Ser Phe Lys Asp Ile Lys Lys Ile Met Glu Glu
                165   170   175
Lys Ile Gln Ile Ser Gly Ser Asn Tyr Lys Ser Leu Glu Val Leu Val
            180   185   190
Ala Asp Leu Val Asn Ala Gln Lys Asp Ser Met Gln Asp Glu Ser Ser
        195   200   205
Gln Thr Ser Leu Gln Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg
    210   215   220
Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala
225   230   235   240
Ile Val Phe Val Pro Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala
                245   250   255
Glu Ala Val Asp Lys Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys
            260   265   270
Gln Lys Ile Phe Met Ser
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<210> 40
<211> 2409
<212> DNA
<213> Homo Sapien

<400> 40
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gatggataa 2409

<210> 41
<211> 802
<212> PRT
<213> Homo Sapien

<400> 41
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Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
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Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
35 40 45
Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Phe
50 55 60
Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn
65 70 75 80
Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
85 90 95

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Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
            100                 105                 110
His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
        115                 120                 125
His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
    130                 135                 140
Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
145                 150                 155                 160
Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Lys Ser
                165                 170                 175
Val Tyr Ser Gly Tyr Ser Arg Lys Pro Val Lys Asn Asn Leu Ala Arg
            180                 185                 190
Ser Gly Asn Glu Glu Lys Met Met Ala Leu Leu Thr Pro Leu Asn Val
        195                 200                 205
Asn Cys His Ala Ser Asp Gly Arg Lys His Gly Ala Cys Val Asn Ala
    210                 215                 220
Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn
225                 230                 235                 240
Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
                245                 250                 255
Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
            260                 265                 270
Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
        275                 280                 285
Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
    290                 295                 300
Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu
305                 310                 315                 320
Lys Leu Cys Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg
                325                 330                 335
Gln Ser Thr Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val
            340                 345                 350
Val Glu Tyr Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
        355                 360                 365
Gly Gly Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
    370                 375                 380
Val Ala Glu Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp
385                 390                 395                 400
Leu Trp Lys Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr
                405                 410                 415
Glu Ile Cys Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys
            420                 425                 430
Asn Arg Asp Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr
        435                 440                 445
Asp Ile Gln Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala
    450                 455                 460
Lys Lys Gly Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn
465                 470                 475                 480
Val Asn Cys Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu
                485                 490                 495
Ala Ala Gly Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His
            500                 505                 510
Gly Ala Asp Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His
        515                 520                 525
Asn Ala Ala Ser Tyr Gly Ile Thr Leu Asp Val Leu Val Glu Met Gly
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530 535 540
His Lys Glu Leu Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His
545 550 555 560
Lys Leu Ile Lys Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu
565 570 575
Asn Pro Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile
580 585 590
Asp Leu Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met
595 600 605
Gln Ser Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile
610 615 620
Phe Asn Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys
625 630 635 640
Leu Trp Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn
645 650 655
His Asn His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val
660 665 670
Asn Ala Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly
675 680 685
Gly Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
690 695 700
Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His
705 710 715 720
Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg
725 730 735
Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala
740 745 750
His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn
755 760 765
Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr
770 775 780
Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
785 790 795 800
Asp Gly

<210> 42
<211> 5175
<212> DNA
<213> Homo Sapien

<400> 42
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caccttgctt ccaaagaagg ccatgtagag gttgtttctg agctgctgca gagagaagcc 180
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caagcagagg tggtaaaagt cttggttaca aatggagcca atgtcaatgc acaatctcag 300
aatggtttca cgccattgta tatggcagcc caggaaaatc acctggaagt tgtcaagttt 360
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<210> 43
<211> 1724
<212> PRT
<213> Homo Sapien

<400> 43

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            20                  25                  30
Asn Gln Asn Gly Leu Asn Ala Leu His Leu Ala Ser Lys Glu Gly His
        35                  40                  45
Val Glu Val Val Ser Glu Leu Leu Gln Arg Glu Ala Asn Val Asp Ala
    50                  55                  60
Ala Thr Lys Lys Gly Asn Thr Ala Leu His Ile Ala Ser Leu Ala Gly
65                  70                  75                  80
Gln Ala Glu Val Val Lys Val Leu Val Thr Asn Gly Ala Asn Val Asn
                85                  90                  95
Ala Gln Ser Gln Asn Gly Phe Thr Pro Leu Tyr Met Ala Ala Gln Glu
            100                 105                 110
Asn His Leu Glu Val Val Lys Phe Leu Leu Asp Asn Gly Ala Ser Gln
        115                 120                 125
Ser Leu Ala Thr Glu Asp Gly Phe Thr Pro Leu Ala Val Ala Leu Gln
    130                 135                 140
Gln Gly His Asp Gln Val Val Ser Leu Leu Leu Glu Asn Asp Thr Lys
145                 150                 155                 160
Gly Lys Val Arg Leu Pro Ala Leu His Ile Ala Ala Arg Lys Asp Asp
                165                 170                 175
Thr Lys Ala Ala Ala Leu Leu Leu Gln Asn Asp Asn Asn Ala Asp Val
            180                 185                 190
Glu Ser Lys Ser Gly Phe Thr Pro Leu His Ile Ala Ala His Tyr Gly
        195                 200                 205
Asn Ile Asn Val Ala Thr Leu Leu Leu Asn Arg Ala Ala Ala Val Asp
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    210                 215                 220
Phe Thr Ala Arg Asn Asp Ile Thr Pro Leu His Val Ala Ser Lys Arg
225                 230                 235                 240
Gly Asn Ala Asn Met Val Lys Leu Leu Leu Asp Arg Gly Ala Lys Ile
                245                 250                 255
Asp Ala Lys Thr Arg Asp Gly Leu Thr Pro Leu His Cys Gly Ala Arg
            260                 265                 270
Ser Gly His Glu Gln Val Val Glu Met Leu Leu Asp Arg Ala Ala Pro
        275                 280                 285
Ile Leu Ser Lys Thr Lys Asn Gly Leu Ser Pro Leu His Met Ala Thr
    290                 295                 300
Gln Gly Asp His Leu Asn Cys Val Gln Leu Leu Leu Gln His Asn Val
305                 310                 315                 320
Pro Val Asp Asp Val Thr Asn Asp Tyr Leu Thr Ala Leu His Val Ala
                325                 330                 335
Ala His Cys Gly His Tyr Lys Val Ala Lys Val Leu Leu Asp Lys Lys
            340                 345                 350
Ala Asn Pro Asn Ala Lys Ala Leu Asn Gly Phe Thr Pro Leu His Ile
        355                 360                 365
Ala Cys Lys Lys Asn Arg Ile Lys Val Met Glu Leu Leu Leu Lys His
    370                 375                 380
Gly Ala Ser Ile Gln Ala Val Thr Glu Arg Gly Glu Thr Ala Leu His
385                 390                 395                 400
Met Ala Ala Arg Ser Gly Gln Ala Glu Val Val Arg Tyr Leu Val Gln
                405                 410                 415
Asp Gly Ala Gln Val Glu Ala Lys Ala Lys Asp Asp Gln Thr Pro Leu
            420                 425                 430
His Ile Ser Ala Arg Leu Gly Lys Ala Asp Ile Val Gln Gln Leu Leu
        435                 440                 445
Gln Gln Gly Ala Ser Pro Asn Ala Ala Thr Thr Ser Gly Tyr Thr Pro
    450                 455                 460
Leu His Leu Ser Ala Arg Glu Gly His Glu Asp Val Ala Ala Phe Leu
465                 470                 475                 480
Leu Asp His Gly Ala Ser Leu Ser Ile Thr Thr Lys Ser Gly Leu Thr
                485                 490                 495
Pro Leu His Val Ala Ala His Tyr Asp Asn Gln Lys Val Ala Leu Leu
            500                 505                 510
Leu Leu Asp Gln Gly Ala Ser Pro His Ala Ala Ala Lys Asn Gly Tyr
        515                 520                 525
Thr Pro Leu His Ile Ala Ala Lys Lys Asn Gln Met Asp Ile Ala Thr
    530                 535                 540
Thr Leu Leu Glu Tyr Gly Ala Asp Ala Asn Ala Val Thr Arg Gln Gly
545                 550                 555                 560
Ile Ala Ser Val His Leu Ala Ala Gln Glu Gly His Val Asp Met Val
                565                 570                 575
Ser Leu Leu Leu Gly Arg Asn Ala Asn Val Asn Leu Ser Asn Lys Ser
            580                 585                 590
Gly Leu Thr Pro Leu His Leu Ala Ala Gln Glu Asp Arg Val Asn Val
        595                 600                 605
Ala Glu Val Leu Val Asn Gln Gly Ala His Val Asp Ala Gln Thr Lys
    610                 615                 620
Val Tyr Gly Pro Pro Leu Pro His Gly Lys Glu Cys Val His Leu Val
625                 630                 635                 640
Thr Ala Asn Gly Tyr Thr Pro Leu His Gln Ala Ala Gln Gln Gly His
                645                 650                 655
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Thr His Ile Ile Asn Val Leu Leu Gln Asn Asn Ala Ser Pro Asn Glu
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Leu Thr Val Thr Val Thr Glu Lys His Lys Met Asn Val Pro Glu Thr
675 680 685
Met Asn Glu Val Leu Asp Met Ser Asp Asp Glu Val Arg Lys Ala Asn
690 695 700
Ala Pro Glu Met Leu Ser Asp Gly Glu Tyr Ile Ser Asp Val Glu Glu
705 710 715 720
Gly Asn Arg Cys Thr Trp Tyr Lys Ile Pro Lys Val Gln Glu Phe Thr
725 730 735
Val Lys Thr Asp Thr Phe Lys Arg Glu Ala Phe Asp Val Gly Leu Leu
740 745 750
Ser Thr Ser Ala Gly Glu Asp Ala Met Thr Gly Asp Thr Asp Lys Tyr
755 760 765
Leu Gly Pro Gln Asp Leu Lys Glu Leu Gly Asp Asp Ser Leu Pro Ala
770 775 780
Glu Gly Tyr Met Gly Phe Ser Leu Gly Ala Arg Ser Ala Arg Phe Leu
785 790 795 800
Val Ser Phe Met Val Asp Ala Arg Gly Gly Ser Met Arg Gly Ser Arg
805 810 815
His His Gly Met Arg Ile Ile Ile Pro Pro Arg Lys Cys Thr Ala Pro
820 825 830
Thr Arg Ile Thr Cys Arg Leu Val Lys Arg His Lys Leu Ala Asn Pro
835 840 845
Pro Pro Met Val Glu Gly Glu Gly Leu Ala Ser Arg Leu Val Glu Met
850 855 860
Gly Pro Ala Gly Ala Gln Phe Leu Gly Pro Val Ile Val Glu Ile Pro
865 870 875 880
His Phe Gly Ser Met Arg Gly Lys Glu Arg Glu Leu Ile Val Leu Arg
885 890 895
Ser Glu Asn Gly Glu Thr Trp Lys Glu His Gln Phe Asp Ser Lys Asn
900 905 910
Glu Asp Leu Thr Glu Leu Leu Asn Gly Met Asp Glu Glu Leu Asp Ser
915 920 925
Pro Glu Glu Leu Gly Lys Lys Arg Ile Cys Arg Ile Ile Thr Lys Asp
930 935 940
Phe Pro Gln Tyr Phe Ala Val Val Ser Arg Ile Lys Gln Glu Ser Asn
945 950 955 960
Gln Ile Gly Pro Glu Gly Gly Ile Leu Ser Ser Thr Thr Val Pro Leu
965 970 975
Val Gln Ala Ser Phe Pro Glu Gly Ala Leu Thr Lys Arg Ile Arg Val
980 985 990
Gly Leu Gln Ala Gln Pro Val Pro Asp Glu Ile Val Lys Lys Ile Leu
995 1000 1005
Gly Asn Lys Ala Thr Phe Ser Pro Ile Val Thr Val Glu Pro Arg Arg
1010 1015 1020
Arg Lys Phe His Lys Pro Ile Thr Met Thr Ile Pro Val Pro Pro Pro
1025 1030 1035 1040
Ser Gly Glu Gly Val Ser Asn Gly Tyr Lys Gly Asp Thr Thr Pro Asn
1045 1050 1055
Leu Arg Leu Leu Cys Ser Ile Thr Gly Gly Thr Ser Pro Ala Gln Trp
1060 1065 1070
Glu Asp Ile Thr Gly Thr Thr Pro Leu Thr Phe Ile Lys Asp Cys Val
1075 1080 1085
Ser Phe Thr Thr Asn Val Ser Ala Arg Tyr Gly Asn Lys Gly Phe Gln

1090 1095 1100

Lys Ala Val Leu Glu Gly Lys Pro Ile Tyr Val Asp Cys Tyr Gly Asn
1105 1110 1115 1120

Leu Ala Pro Leu Thr Lys Gly Gly Gln Gln Leu Val Phe Asn Phe Tyr
1125 1130 1135

Ser Phe Lys Glu Asn Arg Leu Pro Phe Ser Ile Lys Ile Arg Asp Thr
1140 1145 1150

Ser Gln Glu Pro Cys Gly Arg Leu Ser Phe Leu Lys Glu Pro Lys Thr
1155 1160 1165

Thr Lys Gly Leu Pro Gln Thr Ala Val Cys Asn Leu Asn Ile Thr Leu
1170 1175 1180

Pro Ala His Lys Lys Ile Glu Lys Thr Asp Arg Arg Gln Ser Phe Ala
1185 1190 1195 1200

Ser Leu Ala Leu Arg Lys Arg Tyr Ser Tyr Leu Thr Glu Pro Gly Met
1205 1210 1215

Lys Glu Lys Lys Met Gln Ser Glu Leu Ser Asp Glu Glu Glu Ser Thr
1220 1225 1230

Ser Arg Asn Thr Ser Leu Ser Glu Thr Ser Arg Gly Gly Gln Pro Ser
1235 1240 1245

Val Thr Thr Lys Ser Ala Arg Asp Lys Lys Thr Glu Ala Ala Pro Leu
1250 1255 1260

Lys Ser Lys Ser Glu Lys Ala Gly Ser Glu Lys Arg Ser Ser Arg Arg
1265 1270 1275 1280

Thr Ala Asp Ala Leu Thr Ser Val Leu Thr Lys Ile Asn Arg Ile Asp
1285 1290 1295

Ile Val Thr Leu Leu Glu Gly Pro Ile Phe Asp Tyr Gly Asn Ile Ser
1300 1305 1310

Gly Thr Arg Ser Phe Ala Asp Glu Asn Asn Val Phe His Asp Pro Val
1315 1320 1325

Asp Gly Tyr Pro Ser Leu Gln Val Glu Leu Glu Thr Pro Thr Gly Leu
1330 1335 1340

His Tyr Thr Pro Pro Thr Pro Phe Gln Gln Asp Asp Tyr Phe Ser Asp
1345 1350 1355 1360

Ile Ser Ser Ile Glu Ser Pro Leu Arg Thr Pro Ser Arg Leu Ser Asp
1365 1370 1375

Gly Leu Val Pro Ser Gln Gly Asn Ile Glu His Ser Ala Asp Gly Pro
1380 1385 1390

Pro Val Val Thr Ala Glu Asp Ala Ser Leu Glu Asp Ser Lys Leu Glu
1395 1400 1405

Asp Ser Val Pro Leu Thr Glu Met Pro Glu Ala Val Asp Val Asp Glu
1410 1415 1420

Ser Gln Leu Glu Asn Val Cys Leu Ser Glu Tyr Pro Gln Tyr Leu Gly
1425 1430 1435 1440

Asn Leu Ala Gly Ser Pro Lys Asp Val Lys Pro Ala Glu Pro Arg Lys
1445 1450 1455

Leu Gly Val Ser Ser Glu Gln Gln Glu Lys Gly Lys Ser Gly Pro Asp
1460 1465 1470

Glu Glu Met Met Glu Glu Lys Leu Lys Ser Leu Phe Glu Asp Ile Gln
1475 1480 1485

Leu Glu Glu Gly Val Glu Ser Glu Glu Met Thr Glu Glu Lys Val Gln
1490 1495 1500

Ala Ile Leu Lys Arg Val Gln Gln Ala Glu Leu Glu Met Ser Ser Ile
1505 1510 1515 1520

Thr Gly Trp Gln Asn Glu Thr Ser Ser Gly Asn Leu Glu Ser Cys Ala
1525 1530 1535

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Gln Ala Arg Arg Val Thr Gly Gly Leu Leu Asp Arg Leu Asp Asp Ser
            1540                1545                1550
Pro Asp Gln Cys Arg Asp Ser Ile Thr Ser Tyr Leu Lys Gly Glu Ala
        1555                1560                1565
Gly Lys Phe Glu Ala Asn Gly Ser His Thr Glu Ile Thr Pro Glu Ala
    1570                1575                1580
Lys Thr Lys Ser Tyr Phe Pro Glu Ser Gln Asn Asp Val Gly Lys Gln
1585                1590                1595                1600
Ser Thr Lys Glu Thr Leu Lys Pro Lys Ile His Gly Ser Gly His Val
                1605                1610                1615
Glu Glu Pro Ala Ser Pro Leu Ala Ala Tyr Gln Lys Ser Leu Glu Glu
            1620                1625                1630
Thr Ser Lys Leu Ile Ile Glu Glu Thr Lys Pro Cys Val Pro Asp Leu
        1635                1640                1645
Lys Asp Ser Glu Ser Asp Ser Ser Ser Glu Glu Glu Arg Arg Val Thr
    1650                1655                1660
Thr Arg Val Ile Arg Arg Arg Leu Ile Ile Lys Gly Glu Glu Ala Lys
1665                1670                1675                1680
Asn Ile Pro Gly Glu Ser Val Thr Glu Glu Gln Phe Thr Asp Glu Glu
                1685                1690                1695
Gly Asn Leu Ile Thr Arg Lys Gly Glu Gly Phe Lys Val Lys Thr Lys
            1700                1705                1710
Lys Glu Ile Arg His Val Glu Lys Lys Ser His Ser
        1715                1720
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<210> 44
<211> 1305
<212> DNA
<213> Homo Sapien

<400> 44

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<210> 45

<211> 434
<212> PRT
<213> Homo Sapien

<400> 45

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            20                  25                  30
Glu Glu Asn Leu Thr Trp Ser Ser Ser Gly Gly Asp Glu Lys Phe Met
        35                  40                  45
Thr Ser Gly Phe Glu Asp Lys Gln Ser Thr Cys Glu Thr Lys Glu Gln
    50                  55                  60
Glu Pro Lys Leu Val Lys Pro Lys Lys Lys Arg Arg Lys Lys Ser Val
65                  70                  75                  80
Tyr Thr Val Gly Leu Arg Gly Leu Ile Asn Leu Gly Asn Thr Cys Phe
                85                  90                  95
Met Asn Cys Ile Val Gln Ala Leu Thr His Ile Pro Leu Leu Lys Asp
            100                 105                 110
Phe Phe Leu Ser Asp Lys His Lys Cys Ile Met Thr Ser Pro Ser Leu
        115                 120                 125
Cys Leu Val Cys Glu Met Ser Ser Leu Phe His Ala Met Tyr Ser Gly
    130                 135                 140
Ser Arg Thr Pro His Ile Pro Tyr Lys Leu Leu His Leu Ile Trp Ile
145                 150                 155                 160
His Ala Glu His Leu Ala Gly Tyr Arg Gln Gln Asp Ala His Glu Phe
                165                 170                 175
Leu Ile Ala Ile Leu Asp Val Leu His Arg His Ser Lys Asp Asp Ser
            180                 185                 190
Gly Gly Gln Glu Ala Asn Asn Pro Asn Cys Cys Asn Cys Ile Ile Asp
        195                 200                 205
Gln Ile Phe Thr Gly Gly Leu Gln Ser Asp Val Thr Cys Gln Ala Cys
    210                 215                 220
His Ser Val Ser Thr Thr Ile Asp Pro Cys Trp Asp Ile Ser Leu Asp
225                 230                 235                 240
Leu Pro Gly Ser Cys Ala Thr Phe Asp Ser Gln Asn Pro Glu Arg Ala
                245                 250                 255
Asp Ser Thr Val Ser Arg Asp Asp His Ile Pro Gly Ile Pro Ser Leu
            260                 265                 270
Thr Asp Cys Leu Gln Trp Phe Thr Arg Pro Glu His Leu Gly Ser Ser
        275                 280                 285
Ala Lys Ile Lys Cys Asn Ser Cys Gln Ser Tyr Gln Glu Ser Thr Lys
    290                 295                 300
Gln Leu Thr Met Lys Lys Leu Pro Ile Val Ala Cys Phe His Leu Lys
305                 310                 315                 320
Arg Phe Glu His Val Gly Lys Gln Arg Arg Lys Ile Asn Thr Phe Ile
                325                 330                 335
Ser Phe Pro Leu Glu Leu Asp Met Thr Pro Phe Leu Ala Ser Thr Lys
            340                 345                 350
Glu Ser Arg Met Lys Glu Gly Gln Pro Pro Thr Asp Cys Val Pro Asn
        355                 360                 365
Glu Asn Lys Tyr Ser Leu Phe Ala Val Ile Asn His His Gly Thr Leu
    370                 375                 380
Glu Ser Gly His Tyr Thr Ser Phe Ile Arg Gln Gln Lys Asp Gln Trp
385                 390                 395                 400
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Leu Tyr Ser Glu Gly Tyr Leu Leu Phe Tyr His Lys Gln Gly Leu Glu
420 425 430
Lys Asp

<210> 46
<211> 1337
<212> DNA
<213> Homo Sapien

<400> 46
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<210> 47
<211> 444
<212> PRT
<213> Homo Sapien

<400> 47
Ser Asn Ser His Pro Pro Val Ile Ala Thr Thr Val Val Ser Leu Lys
1 5 10 15
Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser Ser Gly Ser Ala Arg Ser
20 25 30
Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys Cys Thr Val Ala Thr Tyr
35 40 45
Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala Ile Ala Ala Gly Thr Thr
50 55 60
Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys Pro Ala Asn Gln Met Val
65 70 75 80
Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser Pro Ser Ser Gly Val Gly
85 90 95

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Ser Pro Val Ser Gly Thr Pro Lys Gln Leu Ala Ser Ile Lys Ile Ile
            100                 105                 110
Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr Lys Cys Ser Lys Ser His
        115                 120                 125
Leu Pro Ser Gln Gly Pro Val Ile Ile Asp Cys Arg Pro Phe Met Glu
    130                 135                 140
Tyr Asn Lys Ser His Ile Gln Gly Ala Val His Ile Asn Cys Ala Asp
145                 150                 155                 160
Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly Lys Ile Thr Val Leu Asp
                165                 170                 175
Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser Phe Lys Arg Ile Phe Ser
            180                 185                 190
Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr Asn Glu Pro Ser Arg Val
        195                 200                 205
Met Pro Ser Gln Pro Leu His Ile Val Leu Glu Ser Leu Lys Arg Glu
    210                 215                 220
Gly Lys Glu Pro Leu Val Leu Lys Gly Gly Leu Ser Ser Phe Lys Gln
225                 230                 235                 240
Asn His Glu Asn Leu Cys Asp Asn Ser Leu Gln Leu Gln Glu Cys Arg
                245                 250                 255
Glu Val Gly Gly Gly Ala Ser Ala Ala Ser Ser Leu Leu Pro Gln Pro
            260                 265                 270
Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala Glu Leu Thr Pro Ile Leu
        275                 280                 285
Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp Ala Gln Asp Leu Asp Thr
    290                 295                 300
Met Gln Arg Leu Asn Ile Gly Tyr Val Ile Asn Val Thr Thr His Leu
305                 310                 315                 320
Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe Asn Tyr Lys Arg Leu Pro
                325                 330                 335
Ala Thr Asp Ser Asn Lys Gln Asn Leu Arg Gln Tyr Phe Glu Glu Ala
            340                 345                 350
Phe Glu Phe Ile Glu Glu Ala His Gln Cys Gly Lys Gly Leu Leu Ile
        355                 360                 365
His Cys Gln Ala Gly Val Ser Arg Ser Ala Thr Ile Val Ile Ala Tyr
    370                 375                 380
Leu Met Lys His Thr Arg Met Thr Met Thr Asp Ala Tyr Lys Phe Val
385                 390                 395                 400
Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn Leu Asn Phe Met Gly Gln
                405                 410                 415
Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn Gly Val Thr Pro Arg Ile
            420                 425                 430
Leu Thr Pro Lys Leu Met Gly Val Glu Thr Val Val
        435                 440
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<210> 48
<211> 3378
<212> DNA
<213> Homo Sapien

<400> 48
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agccctggcc gtgaccttcc accatttgag gatgagtccg aggggctcct aggcacagag 180
gggcccctgg aggaagaaga ggatggagag gagctcattg gagatggcat ggaaagggac 240

taccgcgcca tcccagagct ggacgcctat gaggccgagg gactggctct ggatgatgag 300
gacgtagagg agctgacggc cagtcagagg gaggcagcag agcgggccat gcggcagcgt 360
gaccgggagg ctggccgggg cctgggccgc atgcgccgtg ggctcctgta tgacagcgat 420
gaggaggacg aggagcgccc tgcccgcaag cgccgccagg tggagcgggc cacggaggac 480
ggcgaggagg acgaggagat gattgagagc atcgagaacc tggaggatct caaaggccac 540
tctgtgcgcg agtgggtgag catggcgggc ccccggctgg agatccacca ccgcttcaag 600
aacttcctgc gcactcacgt cgacagccac ggccacaacg tcttcaagga gcgcatcagc 660
gacatgtgca aagagaaccg tgagagcctg gtggtgaact atgaggactt ggcagccagg 720
gagcacgtgc tggcctactt cctgcctgag gcaccggcgg agctgctgca gatctttgat 780
gaggctgccc tggaggtggt actggccatg taccccaagt acgaccgcat caccaaccac 840
atccatgtcc gcatctccca cctgcctctg gtggaggagc tgcgctcgct gaggcagctg 900
catctgaacc agctgatccg caccagtggg gtggtgacca gctgcactgg cgtcctgccc 960
cagctcagca tggtcaagta caactgcaac aagtgcaatt tcgtcctggg tcctttctgc 1020
cagtcccaga accaggaggt gaaaccaggc tcctgtcctg agtgccagtc ggccggcccc 1080
tttgaggtca acatggagga gaccatctat cagaactacc agcgtatccg aatccaggag 1140
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gatctggtgg acagctgcaa gccaggagac gagatagagc tgactggcat ctatcacaac 1260
aactatgatg gctccctcaa cactgccaat ggcttccctg tctttgccac tgtcatccta 1320
gccaaccacg tggccaagaa ggacaacaag gttgctgtag gggaactgac cgatgaagat 1380
gtgaagatga tcactagcct ctccaaggat cagcagatcg gagagaagat ctttgccagc 1440
attgctcctt ccatctatgg tcatgaagac atcaagagag gcctggctct ggccctgttc 1500
ggaggggagc ccaaaaaccc aggtggcaag cacaaggtac gtggtgatat caacgtgctc 1560
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caggctcgct gcacggtcat tgctgccgcc aaccccatag gagggcgcta cgacccctcg 1920
ctgactttct ctgagaacgt ggacctcaca gagcccatca tctcacgctt tgacatcctg 1980
tgtgtggtga gggacaccgt ggacccagtc caggacgaga tgctggcccg cttcgtggtg 2040
ggcagccacg tcagacacca ccccagcaac aaggaggagg aggggctggc caatggcagc 2100
gctgctgagc ccgccatgcc caacacgtat ggcgtggagc ccctgcccca ggaggtcctg 2160
aagaagtaca tcatctacgc caaggagagg gtccacccga agctcaacca gatggaccag 2220
gacaaggtgg ccaagatgta cagtgacctg aggaaagaat ctatggcgac aggcagcatc 2280
cccattacgg tgcggcacat cgagtccatg atccgcatgg cggaggccca cgcgcgcatc 2340
catctgcggg actatgtgat cgaagacgac gtcaacatgg ccatccgcgt gatgctggag 2400
agcttcatag acacacagaa gttcagcgtc atgcgcagca tgcgcaagac ttttgcccgc 2460
tacctttcat tccggcgtga caacaatgag ctgttgctct tcatactgaa gcagttagtg 2520
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ctagggtcag ggcttatagc aggatgtctg gctgcacctg gcatgactgt ttgtttctcc 2880
aagcctgctt tgtgcttctc acctttgggt gggatgcctt gccagtgtgt cttacttggt 2940
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gctgagttca ggatgcctgc gtgtggttta ggtgttagcc ttcttacatg gatgtcagga 3060
gagctgctgc cctcttggcg tgagttgcgt attcaggctg cttttgctgc ctttggccag 3120
agagctggtt gaagatgttt gtaatcgttt tcagtctcct gcaggtttct gtgcccctgt 3180
ggtggaagag ggcacgacag tgccagcgca gcgttctggg ctcctcagtc gcaggggtgg 3240
gatgtgagtc atgcggatta tccactcgcc acagttatca gctgccattg ctccctgtct 3300
gtttccccac tctcttattt gtgcattcgg tttggtttct gtagttttaa tttttaataa 3360
agttgaataa aatataaa 3378

<210> 49

<211> 904
<212> PRT
<213> Homo Sapien

<400> 49

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Leu Gln Glu Ser Ser Glu Ser Phe Thr Met Ala Ser Ser Pro Ala Gln
 1               5                  10                  15
Arg Arg Arg Gly Asn Asp Pro Leu Thr Ser Ser Pro Gly Arg Ser Ser
            20                  25                  30
Arg Arg Thr Asp Ala Leu Thr Ser Ser Pro Gly Arg Asp Leu Pro Pro
        35                  40                  45
Phe Glu Asp Glu Ser Glu Gly Leu Leu Gly Thr Glu Gly Pro Leu Glu
    50                  55                  60
Glu Glu Glu Asp Gly Glu Glu Leu Ile Gly Asp Gly Met Glu Arg Asp
65                  70                  75                  80
Tyr Arg Ala Ile Pro Glu Leu Asp Ala Tyr Glu Ala Glu Gly Leu Ala
                85                  90                  95
Leu Asp Asp Glu Asp Val Glu Glu Leu Thr Ala Ser Gln Arg Glu Ala
            100                 105                 110
Ala Glu Arg Ala Met Arg Gln Arg Asp Arg Glu Ala Gly Arg Gly Leu
        115                 120                 125
Gly Arg Met Arg Arg Gly Leu Leu Tyr Asp Ser Asp Glu Glu Asp Glu
    130                 135                 140
Glu Arg Pro Ala Arg Lys Arg Arg Gln Val Glu Arg Ala Thr Glu Asp
145                 150                 155                 160
Gly Glu Glu Asp Glu Glu Met Ile Glu Ser Ile Glu Asn Leu Glu Asp
                165                 170                 175
Leu Lys Gly His Ser Val Arg Glu Trp Val Ser Met Ala Gly Pro Arg
            180                 185                 190
Leu Glu Ile His His Arg Phe Lys Asn Phe Leu Arg Thr His Val Asp
        195                 200                 205
Ser His Gly His Asn Val Phe Lys Glu Arg Ile Ser Asp Met Cys Lys
    210                 215                 220
Glu Asn Arg Glu Ser Leu Val Val Asn Tyr Glu Asp Leu Ala Ala Arg
225                 230                 235                 240
Glu His Val Leu Ala Tyr Phe Leu Pro Glu Ala Pro Ala Glu Leu Leu
                245                 250                 255
Gln Ile Phe Asp Glu Ala Ala Leu Glu Val Val Leu Ala Met Tyr Pro
            260                 265                 270
Lys Tyr Asp Arg Ile Thr Asn His Ile His Val Arg Ile Ser His Leu
        275                 280                 285
Pro Leu Val Glu Glu Leu Arg Ser Leu Arg Gln Leu His Leu Asn Gln
    290                 295                 300
Leu Ile Arg Thr Ser Gly Val Val Thr Ser Cys Thr Gly Val Leu Pro
305                 310                 315                 320
Gln Leu Ser Met Val Lys Tyr Asn Cys Asn Lys Cys Asn Phe Val Leu
                325                 330                 335
Gly Pro Phe Cys Gln Ser Gln Asn Gln Glu Val Lys Pro Gly Ser Cys
            340                 345                 350
Pro Glu Cys Gln Ser Ala Gly Pro Phe Glu Val Asn Met Glu Glu Thr
        355                 360                 365
Ile Tyr Gln Asn Tyr Gln Arg Ile Arg Ile Gln Glu Ser Pro Gly Lys
    370                 375                 380
Val Ala Ala Gly Arg Leu Pro Arg Ser Lys Asp Ala Ile Leu Leu Ala
385                 390                 395                 400
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Asp Leu Val Asp Ser Cys Lys Pro Gly Asp Glu Ile Glu Leu Thr Gly
405 410 415
Ile Tyr His Asn Asn Tyr Asp Gly Ser Leu Asn Thr Ala Asn Gly Phe
420 425 430
Pro Val Phe Ala Thr Val Ile Leu Ala Asn His Val Ala Lys Lys Asp
435 440 445
Asn Lys Val Ala Val Gly Glu Leu Thr Asp Glu Asp Val Lys Met Ile
450 455 460
Thr Ser Leu Ser Lys Asp Gln Gln Ile Gly Glu Lys Ile Phe Ala Ser
465 470 475 480
Ile Ala Pro Ser Ile Tyr Gly His Glu Asp Ile Lys Arg Gly Leu Ala
485 490 495
Leu Ala Leu Phe Gly Gly Glu Pro Lys Asn Pro Gly Gly Lys His Lys
500 505 510
Val Arg Gly Asp Ile Asn Val Leu Leu Cys Gly Asp Pro Gly Thr Ala
515 520 525
Lys Ser Gln Phe Leu Lys Tyr Ile Glu Lys Val Ser Ser Arg Ala Ile
530 535 540
Phe Thr Thr Gly Gln Gly Ala Ser Ala Val Gly Leu Thr Ala Tyr Val
545 550 555 560
Gln Arg His Pro Val Ser Arg Glu Trp Thr Leu Glu Ala Gly Ala Leu
565 570 575
Val Leu Ala Asp Arg Gly Val Cys Leu Ile Asp Glu Phe Asp Lys Met
580 585 590
Asn Asp Gln Asp Arg Thr Ser Ile His Glu Ala Met Glu Gln Gln Ser
595 600 605
Ile Ser Ile Ser Lys Ala Gly Ile Val Thr Ser Leu Gln Ala Arg Cys
610 615 620
Thr Val Ile Ala Ala Ala Asn Pro Ile Gly Gly Arg Tyr Asp Pro Ser
625 630 635 640
Leu Thr Phe Ser Glu Asn Val Asp Leu Thr Glu Pro Ile Ile Ser Arg
645 650 655
Phe Asp Ile Leu Cys Val Val Arg Asp Thr Val Asp Pro Val Gln Asp
660 665 670
Glu Met Leu Ala Arg Phe Val Val Gly Ser His Val Arg His His Pro
675 680 685
Ser Asn Lys Glu Glu Glu Gly Leu Ala Asn Gly Ser Ala Ala Glu Pro
690 695 700
Ala Met Pro Asn Thr Tyr Gly Val Glu Pro Leu Pro Gln Glu Val Leu
705 710 715 720
Lys Lys Tyr Ile Ile Tyr Ala Lys Glu Arg Val His Pro Lys Leu Asn
725 730 735
Gln Met Asp Gln Asp Lys Val Ala Lys Met Tyr Ser Asp Leu Arg Lys
740 745 750
Glu Ser Met Ala Thr Gly Ser Ile Pro Ile Thr Val Arg His Ile Glu
755 760 765
Ser Met Ile Arg Met Ala Glu Ala His Ala Arg Ile His Leu Arg Asp
770 775 780
Tyr Val Ile Glu Asp Asp Val Asn Met Ala Ile Arg Val Met Leu Glu
785 790 795 800
Ser Phe Ile Asp Thr Gln Lys Phe Ser Val Met Arg Ser Met Arg Lys
805 810 815
Thr Phe Ala Arg Tyr Leu Ser Phe Arg Arg Asp Asn Asn Glu Leu Leu
820 825 830
Leu Phe Ile Leu Lys Gln Leu Val Ala Glu Gln Val Thr Tyr Gln Arg

```
        835                 840                 845
Asn Arg Phe Gly Ala Gln Gln Asp Thr Ile Glu Val Pro Glu Lys Asp
    850                 855                 860
Leu Val Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe
865                 870                 875                 880
Tyr Asp Ser Glu Leu Phe Arg Met Asn Lys Phe Ser His Asp Leu Lys
                885                 890                 895
Arg Lys Met Ile Leu Gln Gln Phe
            900
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<210> 50
<211> 2815
<212> DNA
<213> Homo Sapien

<400> 50

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gcctggagcc gacaccaccg ccatcatgcc ggccgtgtcc aagggcgatg ggatgcgggg      60
gctcgcggtg ttcatctccg acatccggaa ctgtaagagc aaagaggcgg aaattaagag     120
aatcaacaag gaactggcca acatccgctc caagttcaaa ggagacaaag ccttggatgg     180
ctacagtaag aaaaaatatg gttacctgtt catttctgtg ctggtgaact cgaactcgga     240
gctgatccgc ctcatcaaca acgccatcaa gaatgacctg gccagccgca accccacctt     300
catgtgcctg gccctgcact gcatcgccaa cgtgggcagc cgggagatgg gcgaggcctt     360
tgccgctgac atcccccgca tcctggtggc cggggacagc atggacagtg tcaagcagag     420
tgcggccctg tgcctccttc gactgtacaa ggcctcgcct gacctggtgc ccatgggcga     480
gtggacggcg cgtgtggtac acctgctcaa tgaccagcac atgggtgtgg tcacggccgc     540
cgtcagcctc atcacctgtc tctgcaagaa gaacccagat gacttcaaga cgtgcgtctc     600
tctggctgtg tcgcgcctga gccggatcgt ctcctctgcc tccaccgacc tccaggacta     660
cacctactac ttcgtcccag caccctggct ctcggtgaag ctcctgcggc tgctgcagtg     720
ctacccgcct ccagaggatg cggctgtgaa ggggcggctg gtggaatgtc tggagactgt     780
gctcaacaag gcccaggagc cccccaaatc caagaaggtg cagcattcca acgccaagaa     840
cgccatcctc ttcgagacca tcagcctcat catccactat gacagtgagc ccaacctcct     900
ggttcgggcc tgcaaccagc tgggccagtt cctgcagcac cgggagacca acctgcgcta     960
cctggccctg gagagcatgt gcacgctggc cagctccgag ttctcccatg aagccgtcaa    1020
gacgcacatt gacaccgtca tcaatgccct caagacggag cgggacgtca gcgtgcggca    1080
gcgggcggct gacctcctct acgccatgtg tgaccggagc aatgccaagc agatcgtgtc    1140
ggagatgctg cggtacctgg agacggcaga ctacgccatc cgcgaggaga tcgtcctgaa    1200
ggtggccatc ctggccgaga agtacgccgt ggactacagc tggtacgtgg acaccatcct    1260
caacctcatc cgcattgcgg gcgactacgt gagtgaggag gtgtggtacc gtgtgctaca    1320
gatcgtcacc aaccgtgatg acgtccaggg ctatgccgcc aagaccgtct ttgaggcgct    1380
ccaggccccc gcctgtcacg agaacatggt gaaggttggc ggctacatcc ttggggagtt    1440
tgggaacctg attgctgggg acccccgctc cagcgtggcc acgcgggcgc tgctgctgtc    1500
cacctacatc aagttcatca acctcttccc cgagaccaag gccaccatcc agggcgtcct    1560
gcgggccggc tcccagctgc gcaatgctga cgtggagctg cagcagcgag ccgtggagta    1620
cctcaccctc agctcagtgg ccagcaccga cgtcctggcc acggtgctgg aggagatgcc    1680
gcccttcccc gagcgcgagt cgtccatcct ggccaagctg aaacgcaaga aggggccagg    1740
ggccggcagc gccctggacg atggccggag ggaccccagc agcaacgaca tcaacggggg    1800
catggagccc acccccagca ctgtgtcgac gccctcgccc tccgccgacc tcctggggct    1860
gcgggcagcc cctcccccgg cagcaccccc ggcttctgca ggagcaggga accttctggt    1920
ggacgtcttc gatggcccgg ccgcccagcc cagcctgggg cccacccccg aggaggcctt    1980
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taagtttgtg tgtaagaaca acggggtcct gttcgagaac cagctgctgc agatcggagt    2100
caagtcagag ttccgacaga acctgggccg catgtatctc ttctatggca acaagacctc    2160
ggtgcagttc cagaatttct cacccactgt ggttcacccg ggagacctcc agactcatat    2220
cctctcaggc ccggcccagc ctcctgcctc tccacgtcgg ccttcctcac cgtggggaag    2280
ccggctgacc cagctggctg tgcagaccaa gcgcgtggcg gcgcaggtgg acggcggcgc    2340
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gcaggtgcag caggtgctca atatcgagtg cctgcgggac ttcctgacgc ccccgctgct    2400
gtccgtgcgc ttccggtacg gtggcgcccc ccaggccctc accctgaagc tcccagtgac    2460
catcaacaag ttcttccagc ccaccgagat ggcggcccag gatttcttcc agcgctggaa    2520
gcagctgagc ctccctcaac aggaggcgca gaaaatcttc aaagccaacc accccatgga    2580
cgcagaagtt actaaggcca agcttctggg gtttggctct gctctcctgg acaatgtgga    2640
ccccaaccct gagaacttcg tgggggcggg gatcatccag actaaagccc tgcaggtggg    2700
ctgtctgctt cggctggagc ccaatgccca ggcccagatg taccggctga ccctgcgcac    2760
cagcaaggag cccgtctccc gtcacctgtg tgagctgctg gcacagcagt tctga         2815

<210> 51
<211> 937
<212> PRT
<213> Homo Sapien

<400> 51
Pro Gly Ala Asp Thr Thr Ala Ile Met Pro Ala Val Ser Lys Gly Asp
 1               5                  10                  15
Gly Met Arg Gly Leu Ala Val Phe Ile Ser Asp Ile Arg Asn Cys Lys
            20                  25                  30
Ser Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala Asn Ile
        35                  40                  45
Arg Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys
    50                  55                  60
Lys Tyr Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu
65                  70                  75                  80
Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg
                85                  90                  95
Asn Pro Thr Phe Met Cys Leu Ala Leu His Cys Ile Ala Asn Val Gly
            100                 105                 110
Ser Arg Glu Met Gly Glu Ala Phe Ala Ala Asp Ile Pro Arg Ile Leu
        115                 120                 125
Val Ala Gly Asp Ser Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys
    130                 135                 140
Leu Leu Arg Leu Tyr Lys Ala Ser Pro Asp Leu Val Pro Met Gly Glu
145                 150                 155                 160
Trp Thr Ala Arg Val Val His Leu Leu Asn Asp Gln His Met Gly Val
                165                 170                 175
Val Thr Ala Ala Val Ser Leu Ile Thr Cys Leu Cys Lys Lys Asn Pro
            180                 185                 190
Asp Asp Phe Lys Thr Cys Val Ser Leu Ala Val Ser Arg Leu Ser Arg
        195                 200                 205
Ile Val Ser Ser Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe
    210                 215                 220
Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys
225                 230                 235                 240
Tyr Pro Pro Pro Glu Asp Ala Ala Val Lys Gly Arg Leu Val Glu Cys
                245                 250                 255
Leu Glu Thr Val Leu Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys
            260                 265                 270
Val Gln His Ser Asn Ala Lys Asn Ala Ile Leu Phe Glu Thr Ile Ser
        275                 280                 285
Leu Ile Ile His Tyr Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys
    290                 295                 300
Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr
305                 310                 315                 320
```

Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His
325 330 335
Glu Ala Val Lys Thr His Ile Asp Thr Val Ile Asn Ala Leu Lys Thr
340 345 350
Glu Arg Asp Val Ser Val Arg Gln Arg Ala Ala Asp Leu Leu Tyr Ala
355 360 365
Met Cys Asp Arg Ser Asn Ala Lys Gln Ile Val Ser Glu Met Leu Arg
370 375 380
Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile Val Leu Lys
385 390 395 400
Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser Trp Tyr Val
405 410 415
Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr Val Ser Glu
420 425 430
Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg Asp Asp Val
435 440 445
Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala
450 455 460
Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe
465 470 475 480
Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Val Ala Thr Arg Ala
485 490 495
Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe Pro Glu Thr
500 505 510
Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln Leu Arg Asn
515 520 525
Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu Thr Leu Ser
530 535 540
Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu Glu Met Pro
545 550 555 560
Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu Lys Arg Lys
565 570 575
Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg Arg Asp Pro
580 585 590
Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro Ser Thr Val
595 600 605
Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg Ala Ala Pro
610 615 620
Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn Leu Leu Val
625 630 635 640
Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly Pro Thr Pro
645 650 655
Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly Pro Pro Ile
660 665 670
Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys Asn Asn Gly
675 680 685
Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys Ser Glu Phe
690 695 700
Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn Lys Thr Ser
705 710 715 720
Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro Gly Asp Leu
725 730 735
Gln Thr His Ile Leu Ser Gly Pro Ala Gln Pro Pro Ala Ser Pro Arg
740 745 750
Arg Pro Ser Ser Pro Trp Gly Ser Arg Leu Thr Gln Leu Ala Val Gln

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        755                 760                 765
Thr Lys Arg Val Ala Ala Gln Val Asp Gly Gly Ala Gln Val Gln Gln
    770                 775                 780
Val Leu Asn Ile Glu Cys Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu
785                 790                 795                 800
Ser Val Arg Phe Arg Tyr Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys
                805                 810                 815
Leu Pro Val Thr Ile Asn Lys Phe Phe Gln Pro Thr Glu Met Ala Ala
            820                 825                 830
Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu
        835                 840                 845
Ala Gln Lys Ile Phe Lys Ala Asn His Pro Met Asp Ala Glu Val Thr
    850                 855                 860
Lys Ala Lys Leu Leu Gly Phe Gly Ser Ala Leu Leu Asp Asn Val Asp
865                 870                 875                 880
Pro Asn Pro Glu Asn Phe Val Gly Ala Gly Ile Ile Gln Thr Lys Ala
                885                 890                 895
Leu Gln Val Gly Cys Leu Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln
            900                 905                 910
Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Pro Val Ser Arg His
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Leu Cys Glu Leu Leu Ala Gln Gln Phe
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<213> Homo sapiens

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        35   40   45
Pro Ala Gly Ser Thr Lys Pro Phe Val His Ala Val Pro Pro Ser Asp
    50   55   60
Pro Leu Arg Gln Ala Asn Arg Leu Pro Ile Lys Val Leu Lys Met Leu
65   70   75   80
Thr Ala Arg Thr Gly His Ile Leu His Pro Glu Tyr Leu Gln Pro Leu
                85   90   95
Pro Ser Thr Pro Val Ser Pro Ile Glu Leu Asp Ala Lys Lys Ser Pro
            100   105   110
Leu Ala Leu Leu Ala Gln Thr Cys Ser Gln Ile Gly Lys Pro Asp Pro
        115   120   125
Ser Pro Ser Ser Lys Leu Ser Ser Val Ala Ser Asn Gly Gly Gly Ala

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    130                 135                 140
Gly Gly Ala Gly Gly Gly Ala Ala Gly Asp Lys Asp Thr Lys Ser Gly
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Pro Tyr Ser Lys Pro Gly Ser Asp Lys Lys Glu Pro Gly Gly Gly Gly
            180                 185                 190
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Val Ser Ser Glu
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Lys Ser Gly Phe Arg Val Pro Ser Ala Thr Cys Gln Pro Phe Thr Pro
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Arg Thr Gly Ser Pro Ser Ser Ser Ala Ser Ala Cys Ser Pro Gly Gly
225                 230                 235                 240
Met Leu Ser Ser Ala Gly Gly Ala Pro Glu Gly Lys Asp Asp Lys Lys
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Asp Thr Asp Val Gly Gly Gly Gly Lys Gly Thr Gly Gly Ala Ser Ala
            260                 265                 270
Glu Gly Gly Pro Thr Gly Leu Ala His Gly Arg Ile Ser Cys Gly Gly
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Gly Ile Asn Val Asp Val Asn Gln His Pro Asp Gly Gly Pro Gly Gly
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Lys Ala Leu Gly Ser Asp Cys Gly Gly Ser Ser Gly Ser Ser Ser Gly
305                 310                 315                 320
Ser Gly Pro Ser Ala Pro Thr Ser Ser Ser Val Leu Gly Ser Gly Leu
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Pro Pro Ala Gly Met Thr Tyr Pro Gly Ser Leu Ala Gly Ala Tyr Ala
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Gly Tyr Pro Pro Gln Phe Leu Pro His Gly Val Ala Leu Asp Pro Thr
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Lys Pro Gly Ser Leu Val Gly Ala Gln Leu Ala Ala Ala Ala Ala Gly
385                 390                 395                 400
Ser Leu Gly Cys Ser Lys Pro Ala Gly Ser Ser Pro Leu Ala Gly Ala
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Ser Pro Pro Ser Val Met Thr Ala Ser Leu Cys Arg Asp Pro Tyr Cys
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Leu Ser Tyr His Cys Ala Ser His Leu Ala Gly Ala Ala Ala Ala Ser
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Ala Ser Cys Ala His Asp Pro Ala Ala Ala Ala Ala Ala Leu Lys Ser
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Gly Tyr Pro Leu Val Tyr Pro Thr His Pro Leu His Gly Val His Ser
465                 470                 475                 480
Ser Leu Thr Ala Ala Ala Ala Ala Gly Ala Thr Pro Pro Ser Leu Ala
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Gly His Pro Leu Tyr Pro Tyr Gly Phe Met Leu Pro Asn Asp Pro Leu
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Pro His Ile Cys Asn Trp Val Ser Ala Asn Gly Pro Cys Asp Lys Arg
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    530                 535                 540
Phe Pro Gly Thr Asp Lys Leu Leu Ser Gly Tyr Pro Ser Ser Ser Ser
545                 550                 555                 560
Leu Ala Ser Ala Ala Ala Ala Ala Met Ala Cys His Met His Ile Pro
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His His Ala Leu Gly Leu Ser Ser Arg Tyr His Pro Tyr Ser Lys Ser
        595                 600                 605
Pro Leu Pro Thr Pro Gly Ala Pro Val Pro Val Pro Ala Ala Thr Gly
    610                 615                 620
Pro Tyr Tyr Ser Pro Tyr Ala Leu Tyr Gly Gln Arg Leu Thr Thr Ala
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Ser Ala Leu Gly Tyr Gln
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Table 1: Genetic modifiers

modifier	flyCT	Start	End	hCG	hCT	hCP	Start	End	E-value	gene name / protein family	comments	SEQ ID NO (hCT/hCP)
EP(2)2107	CT25384	94	183	hCG37225	hCT28457	hCP47994	96	185	4.00E-32	TG-interacting factor / TALE/KNOX homeobox protein	modifier of Dps and C99	6/7
EP(2)2122	CT11970	54	411	hCG22190	hCT13283	hCP39677	12	348	4.00E-75	n/a	modifier of Dps and C99	8/9
EP(2)2151	CT3996	27	392	hCG22926	hCT14025	hCP40373	39	415	1.00E-109	NAP1 / aspartyl protease-related	modifier of C99	10/11
EP(2)2162	CT7676	15	374	hCG30594	hCT21765	hCP44907	13	373	3.00E-97	n/a	modifier of Dps and C99, lethal over C99	12/13
EP(2)2173	CT14619	10	531	hCG23983	hCT15097	hCP41313	100	564	1.00E-25	Drosophila nocA Zn finger transcription factor ortholog	modifier of Dps and C99, human ortholog on 10q	14/15, 16/17, 52/53
EP(2)2205	CT9828	93	619	hCG41821	hCT33094	hCP51674	668	1180	4.00E-66	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 (ACE)	modifier of Dps and C99, metalloprotease	18/19
EP(2)2511	CT11457	6	258	hCG20663	hCT11743	hCP38288	28	2.76E+02	2.00E-65	copper chaperone for superoxide dismutase / superoxide dismutase [CU-ZN]	modifier of Dps and C99	20/21
EP(2)2554	CT10410	6	192	hCG39955	hCT31207	hCP49745	5	198	2.00E-16	glutathione S-transferase theta 1	modifier of Dps and C99	22/23
EP(2)2554	CT10310	15	661	hCG40293	hCT31548	hCP50060	18	617	2.00E-90	intersectin-related	modifier of Dps and C99	24/25
EP(3)3041	CT5336	14	227	hCG42003	hCT33279	hCP51813	29	246	1.00E-39	HSA011916	modifier of Dps and C99	26/27
EP(X)1526	CT10709	7	597	hCG37950	hCT29186	hCP47880	6	519	1.00E-168	protein kinase inhibitor P58-related	modifier of Dps and C99	28/29
P1396=l(2)05206	CT13013	316	655	hCG20435	hCT11514	hCP38090	106	404	2.00E-72	cyclin	modifier of Dps and C99	30/31
P1486=l(3)00090	CT22943	1818	2491	hCG32338	hCT23526	hCP46544	663	1248	2.00E-84	retinoblastoma binding protein-related	modifier of Dps and C99	32/33
P1505=l(3)00643	CT23724	760	1123	hCG40234	hCT31488	hCP50765	131	439	3.00E-63	early growth response 2 (Krox-20 (Drosophila) homolog)	modifier of Dps, human ortholog on 10q	34/35
P1548=l(3)01814	CT24038	75	167	hCG18539	hCT9598	hCP36359	1	93	1.00E-31	n/a	modifier of Dps and C99	36/37
P2093=l(3)j5C8	CT18339	218	438	hCG14845	hCT5866	hCP35211	38	278	6.00E-31	baculoviral IAP repeat-containing 4 / apoptosis inhibitor related	modifier of Dps and C99	38/39
P2093=l(3)j5C8	CT18415	62	293	hCG17907	hCT8961	hCP33787	353	569	2.00E-18	ankyrin-related	modifier of Dps, human homolog on 10q	40/41
P2093=l(3)j5C8	CT18415	50	349	hCG41783	hCT33056	hCP51594	7	307	2.00E-23	ankyrin-3, ankyrin-G	modifier of Dps, human homolog on 10q	42/43
P2104=l(3)j13B3	CT13750	372	733	hCG201263	hCT201265	hCP201588	61	432	1.00E-111	ubiquitin carboxyl-terminal hydrolase	modifier of Dps and C99	44/45
P2121=l(3)j4E1	CT23760	87	283	hCG25031	hCT16153	hCP41935	239	437	2.00E-37	dual specificity protein phosphatase	modifier of Dps and C99	46/47
P2122=l(3)rL074	CT23073	5	879	hCG39269	hCT30519	hCP50592	21	902	0	minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) / DNA replication licensing factor MCM	modifier of Dps and C99	48/49
P2319=l(2)06694	CT13966	1	932	hCG21123	hCT12209	hCP38695	18	937	0	alpha-adaptin	modifier of C99	50/51